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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:56 ; Search time 103.05 Seconds  
(without alignments)  
743.120 Million cell updates/sec

Title: US-09-575-580B-4  
Perfect score: 1048  
Sequence: 1 MEEVDLQPLSATIACHLDP.....RPKXIIQTRRPEYTPHLS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq 16Dec04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	198	5	AAE18911 Human MCI
2	1002.5	95.7	197	5	AAE18915 Human MCI
3	1002.5	95.7	197	8	ADR14119 Human NF-
4	1002.5	95.7	252	7	ADB64738 Human pro
5	920.5	87.8	198	5	AAE18912 Mouse MCI
6	872.5	83.3	197	5	AAE18914 Human MCI
7	872.5	83.3	197	7	ADR25770 Human pro
8	847.5	80.9	242	8	ADR10481 Human pro
9	835.5	79.7	171	2	AAW73898 Human Dow
10	620.5	59.2	234	4	AAB31788 Amino aci
11	620.5	59.2	243	7	ADB64062 Human pro
12	620.5	59.2	255	5	AAW50760 Human Dow
13	620.5	59.2	255	7	ADR37339 Human Dow
14	613.5	58.5	197	5	AAE18913 Mouse MCI
15	609.5	58.2	197	6	ABO07172 Human p33
16	596.5	56.9	192	5	AAE18916 Human MCI
17	596.5	56.9	192	7	ADR37341 Human Dow
18	596	56.9	241	5	AAE18917 Human MCI
19	596	56.9	241	6	ABO07173 Human p53
20	596	56.9	241	7	ADR37342 Human Dow
21	595	56.8	212	5	AAE18918 Human MCI
22	497	47.4	142	3	AAW58452 Lung can
23	439	41.9	111	3	AAW01768 Human sec
24	379.5	36.2	292	4	ABB71467 Drosophil
25	284	27.1	58	4	AAW15671 Peptide #

ALIGNMENTS

RESULT 1

AAE18911  
ID AAE18911 standard; protein; 198 AA.  
XX  
AC AAE18911;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human MCI associated protein #2.  
XX  
KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
heart failure; cardiomyopathy; heart disease; human.  
XX  
OS Homo sapiens.  
XX  
FN WO200204491-A2.  
XX  
PD 17-JAN-2002.  
XX  
PF 06-JUL-2001; 2001WO-US021662.  
XX  
PR 07-JUL-2000; 2000US-0216601P.  
PR 13-FEB-2001; 2001US-00782953.  
XX  
(TEXA ) UNIV TEXAS SYSTEM.  
PA (WILL//) WILLIAMS S R.  
PA (ROTH//) ROTHERMEL B.  
XX  
PI Williams SR, Rothermel B;  
XX  
WPI: 2002-179698/23.  
DR N-PSDB; AAD30152.  
XX

Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound.  
Disclosure; Page 148-149; 174pp; English.  
The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate to transcriptions of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure.

CC Antibodies to MCIP can be used in characterising the MCIP content of  
 CC healthy and diseased tissues and subsequently for determining the  
 CC presence or absence of cardiomyopathy or as predictor of heart disease.  
 CC The present sequence is human MCIP associated protein  
 XX  
 SQ Sequence 198 AA;

Query Match 100.0%; Score 1048; DB 5; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-108;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60  
 Db 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60  
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120  
 Db 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120  
 QY 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180  
 Db 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180  
 QY 181 KPKIOTRRPEYTPIHLS 198  
 Db 181 KPKIOTRRPEYTPIHLS 198

## RESULT 2

AAE18915  
 ID AAE18915 standard; protein; 197 AA.

XX AAE18915;

DT 17-MAY-2002 (first entry)

XX Human MCIP associated protein #2.

XX Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
 KW heart failure; cardiomyopathy; heart disease; human.

XX Homo sapiens.

XX WO200204491-A2.

XX 17-JAN-2002.

XX 06-JUL-2001; 2001WO-US021662.

XX 07-JUL-2000; 2000US-0216601P.

XX 13-FEB-2001; 2001US-00782953.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (WILL/) WILLIAMS S R.

XX (ROTH/) ROTHERMEL B.

XX Williams SR, Rothermel B;

XX WPI; 2002-179698/23.

XX N-PSDB; AAD30156.

XX Screening for modulators of muscle calcineurin interacting protein (MCIP)  
 PT binding, expression or phosphorylation, useful for treating cardiac  
 PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a  
 PT test compound.

XX Example 1; Page 161-162; 174pp; English.

XX The invention relates to muscle calcineurin interacting proteins (MCIPs)  
 CC and nucleic acid molecules encoding such proteins. MCIPs form a physical  
 CC complex with the catalytic subunit of calcineurin and increased levels of  
 CC MCIPs correspond to a reduced ability of calcineurin to stimulate  
 CC transcription of certain target genes. The invention also relates to

CC methods for identifying modulators of MCIP binding, expression or  
 CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin  
 CC may be used for treating cardiac hypertrophy and heart failure.  
 CC Antibodies to MCIP can be used in characterising the MCIP content of  
 CC healthy and diseased tissues and subsequently for determining the  
 CC presence or absence of cardiomyopathy or as predictor of heart disease.  
 CC The present sequence is human MCIP associated protein. Note: This  
 CC sequence has been described as murine MCIP splice variant in the  
 CC specification, however the sequence seems to be a MCIP associated protein

XX Sequence 197 AA;

Query Match 95.7%; Score 1002.5; DB 5; Length 197;  
 Best Local Similarity 96.5%; Pred. No. 8.4e-103;  
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60  
 Db 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60  
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120  
 Db 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120  
 QY 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180  
 Db 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180  
 QY 181 KPKIOTRRPEYTPIHLS 198  
 Db 180 KPKIOTRRPEYTPIHLS 197

## RESULT 3

ADRI4119

ID ADRI4119 standard; protein; 197 AA.

XX ADRI4119;

XX 21-OCT-2004 (first entry)

XX Human NF-kappaB pathway-associated protein SeqID120.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;  
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;  
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
 KW immunosuppressive; vulnery; gene therapy; immune disorder;  
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;  
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
 KW viral replication; host cell survival; evasion of immune response;  
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;  
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;  
 KW autoimmune disorder; hyper immune activity;  
 KW aberrant acute phase response; hypercongenital condition; birth defect;  
 KW necrotic lesion; wound; organ transplant rejection;  
 KW aberrant signal transduction; proliferating disorder; cancer;  
 KW HIV propagation; human.

XX Homo sapiens.

XX WO2004065577-A2.

XX 05-AUG-2004.

XX 13-JAN-2004; 2004WO-US000798.

XX 14-JAN-2003; 2003US-0440068P.

XX 12-MAY-2003; 2003US-0469757P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PI Nadler SG., Neubauer MG, Feder JN, Carman J;  
 XX DR WPI: 2004-562168/54.  
 XX DR N-PSDB; ADR41118.  
 XX XX  
 XX PT New isolated polynucleotides and polypeptides associated with NF-kappaB  
 XX PT pathway, useful for diagnosing, treating, or preventing disorders or  
 XX PT diseases associated with NF-kappaB pathway.  
 XX XX  
 XX PS Claim 6; SEQ ID NO 120; 237pp; English.  
 XX XX  
 XX CC This invention relates to the novel association of protein sequences (and  
 XX CC the genes which encode them) to the NF-kappaB pathway. The invention may  
 XX CC be useful for the production of compounds with an antiinflammatory,  
 XX CC cytosstatic, hepatotropic, virucide, antiarthritic, antirheumatic,  
 XX CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,  
 XX CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or  
 XX CC vulnary activity or for gene therapy. The proteins and nucleotides are  
 XX CC useful for diagnosing, preventing, treating, or ameliorating conditions  
 XX CC or diseases associated with the NF-kappaB pathway. The condition is an  
 XX CC immune disorder, an inflammatory disorder, an inflammatory disorder  
 XX CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
 XX CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
 XX CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic  
 XX CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
 XX CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
 XX CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
 XX CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
 XX CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper  
 XX CC immune activity, disorders related to aberrant acute phase responses,  
 XX CC hypercongenital conditions, birth defects, necrotic lesions, wounds,  
 XX CC organ transplant rejection, conditions related to organ transplant  
 XX CC rejection, disorders related to aberrant signal transduction,  
 XX CC proliferating disorders, cancers and HIV propagation in cells infected  
 XX CC with other viruses. The present sequence is that of a human protein which  
 XX CC is subject to the novel association with the NF-kappaB pathway of the  
 XX CC invention. Note: This sequence does not appear in the specification but  
 XX CC was obtained by the indexer from Genbank.  
 XX XX  
 XX SQ Sequence 197 AA;  
 Query Match 95.7%; Score 1002.5; DB 8; Length 197;  
 Best Local Similarity 96.5%; Pred. No. 8.4e-103;  
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MEEVDLQDLP SATIACHLDP RVFV DGLCR AKFESLRTYDKOTTFQYFKSFKRVIRNFN 60  
 DB 1 MEEVDLQDLP SATIACHLDP RVFV DGLCR AKFESLRTYDKOTTFQYFKSFKRVIRNFN 60  
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTUHLIGSSHLAPPNPKQFLISPPASPPVGVKQV 120  
 DB 61 PFSAADARLQLHKTFLGKEMKLYFAQTUHLIGSSHLAPPNPKQFLISPPASPPVGVKQV 120  
 QY 121 EDATPVINYDLLLYAISKLGPGKGYELHAATDTPPSVVHVHVCSDQNEEEMERMRKP 180  
 DB 121 EDATPVINYDLLLYAISKLGPGKGYELHAATDTPPSVVHVHVCSDQNEEEMERMRKP 180  
 QY 181 KPILITRRPEYTPHLS 198  
 DB 180 KPILITRRPEYTPHLS 197  
 RESULT 4  
 ADB64738 standard; protein; 252 AA.  
 XX ADB64738;  
 XX 04-DEC-2003 (first entry)  
 XX Human protein encoded by clone NT2NE20141040.  
 XX

Human; pharmaceutical, diagnostic; gene therapy; tissue regeneration;  
 cell regeneration; membrane protein; signal transduction-related protein;  
 transcription-related protein; osteoporosis; neurological disease;  
 cancer; tumour.  
 Homo sapiens.  
 EP1308459-A2.  
 07-MAY-2003.  
 28-MAR-2002; 2002EP-00007401.  
 05-NOV-2001; 2001JP-00379298.  
 25-JAN-2002; 2002US-00350978.  
 (HELI-) HELIX RES INST.  
 (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 Yamamoto J, Tsuno Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 WPI: 2003-450961/43.  
 N-PSDB; ADB62768.  
 New polynucleotides and polypeptides, useful for developing a diagnostic  
 marker or medicines for regulation of their expression and activity, or  
 as targets of gene therapy.  
 Claim 1; Page; 222pp; English.  
 The invention discloses a polynucleotide comprising a sequence selected  
 from 1970 fully defined nucleotide sequences which encode novel  
 polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 or its partial peptide, an antibody binding to the polypeptide or peptide  
 of the polynucleotide, immunologically assaying the polypeptide or  
 peptide of the polynucleotide by contacting the polypeptide or peptide  
 with the antibody of the encoded protein, and observing the binding  
 between the two, a transformant carrying the polynucleotide in an  
 expressible manner and an antisense polynucleotide. The oligonucleotide  
 is useful as a primer for synthesising the polynucleotide, or as a probe  
 for detecting the polynucleotide. The polynucleotides and encoded  
 proteins are useful as pharmaceutical agents and many disease-related  
 genes may be included in them, for developing a diagnostic marker or  
 medicines for regulation of their expression and activity, or as targets  
 of gene therapy. The genes are involved in tissue and/or cell  
 regeneration. Membrane proteins, signal transduction-related proteins,  
 transcription-related proteins, disease-related proteins and genes  
 encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 neurological diseases, cancer, tumours). The cDNA may be used to regulate  
 the activity or expression of the encoded protein to treat diseases. The  
 sequence presented is a protein of the invention. Note: Some of the  
 sequence data for this patent is not represented in the printed  
 specification, but is based on sequence information supplied by the  
 European Patent Office.  
 Sequence 252 AA;  
 Query Match 95.7%; Score 1002.5; DB 7; Length 252;  
 Best Local Similarity 96.5%; Pred. No. 1.2e-102;  
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MEEVDLQDLP SATIACHLDP RVFV DGLCR AKFESLRTYDKOTTFQYFKSFKRVIRNFN 60  
 DB 56 MEEVDLQDLP SATIACHLDP RVFV DGLCR AKFESLRTYDKOTTFQYFKSFKRVIRNFN 115  
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTUHLIGSSHLAPPNPKQFLISPPASPPVGVKQV 120  
 DB 116 PFSAADARLQLHKTFLGKEMKLYFAQTUHLIGSSHLAPPNPKQFLISPPASPPVGVKQV 175  
 QY 121 EDATPVINYDLLLYAISKLGPGKGYELHAATDTPPSVVHVHVCSDQNEEEMERMRKP 180



QY 11 SATIACHLDPVRVFDGLCRKAKESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLR 70  
Db 11 SSLIACVANSDFSESETRAKFESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLRQ 70  
QY 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130  
Db 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130  
QY 131 LLYAISKLGPGKGYELHAAATDPTPSVVHVCSDDQNEEEEEEMERMKRPKPKIIOTRRP 190  
Db 131 LLYAISKLGPGKGYELHAAATDPTPSVVHVCSDDQNEEEEEEMERMKRPKPKIIOTRRP 189  
QY 191 EYTPHLS 198  
Db 190 EYTPHLS 197  
RESULT 7  
ADE25770  
ID ADE25770 standard; protein; 197 AA.  
AC ADE25770;  
XX  
DT 29-JAN-2004 (first entry)  
DE Human protein differentially expressed in foam cells #47.  
KW Human; differential expression; foam cell; LPS; lipopolysaccharide;  
KW cardiovascular disease; atherosclerosis.  
OS Homo sapiens.  
XX  
PN US2003194721-A1.  
PD 16-OCT-2003.  
XX  
PF 18-SEP-2002; 2002US-00247671.  
XX  
PR 19-SEP-2001; 2001US-0323784P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Mikita T, Shiffman D, Porter JG, Kaser MR;  
XX  
WPI: 2003-875398/81.  
DR N-PSDB; ADE25696.  
XX  
PT Combination containing several polynucleotide that are differentially  
PT expressed in foam cells and complements of the polynucleotides, useful  
PT for diagnosing cardiovascular disease or atherosclerosis.  
XX  
PS Disclosure; SEQ ID NO 174; 37pp; English.  
XX  
CC The invention relates to a combination comprising several polynucleotides  
CC having any one of 127 sequences (S1) such as the sequence of human  
CC calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4  
CC hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit  
CC mRNA, etc., and their complements. The cDNAs are differentially expressed  
CC in LPS (lipopolysaccharide)-treated foam cells. Also included are  
CC obtaining an extended or full length gene from a library of nucleic acid  
CC sequences, an expression vector containing the nucleic acids, a host cell  
CC containing the vector, a purified polypeptide appearing as ADE25750 and  
CC ADE25751, producing a protein by culturing the host cell, and a  
CC composition comprising a purified antibody that specifically binds to the  
CC proteins. The foam cell-expressed nucleic acids are useful for a high  
CC throughput detection of differential expression of one or more  
CC polynucleotides in a sample. The sample is from a subject with  
CC atherosclerosis and comparison with a standard defines early, mid or late  
CC stages of the disorder. The foam cell-expressed nucleic acids are useful  
CC to identify a ligand which binds a polynucleotide. The library is chosen  
CC from DNA molecules, peptides, proteins and RNA molecules. The protein is  
CC useful for a high throughput screening of library of molecules or

CC compounds to identify at least one ligand which specifically binds a  
CC protein, for purifying a ligand from a sample for making an antibody. The  
CC foam cell-expressed nucleic acids are useful for diagnosing  
CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful  
CC as elements on a microarray which can be used for detecting related  
CC polynucleotide in a sample, diagnosing cardiovascular disease,  
CC atherosclerosis. The present sequence represents a protein differentially  
CC expressed in LPS treated foam cells.  
XX  
SQ Sequence 197 AA;  
Query Match 83.3%; Score 872.5; DB 7; Length 197;  
Best Local Similarity 89.4%; Pred. No. 2.5e-88;  
Matches 168; Conservative 7; Mismatches 12; Indels 1; Gaps 1;  
QY 11 SATIACHLDPVRVFDGLCRKAKESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLR 70  
Db 11 SSLIACVANSDFSESETRAKFESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLRQ 70  
QY 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130  
Db 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130  
QY 131 LLYAISKLGPGKGYELHAAATDPTPSVVHVCSDDQNEEEEEEMERMKRPKPKIIOTRRP 190  
Db 131 LLYAISKLGPGKGYELHAAATDPTPSVVHVCSDDQNEEEEEEMERMKRPKPKIIOTRRP 189  
QY 191 EYTPHLS 198  
Db 190 EYTPHLS 197  
RESULT 8  
ADR10481  
ID ADR10481 standard; protein; 242 AA.  
XX  
AC ADR10481;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Human protein useful for treating neurological disease Seq 3987.  
XX  
KW human; oligo-capping method; diagnostic marker; gene therapy;  
KW osteoporosis; neurological disease; Alzheimer's disease;  
KW Parkinson's disease; dementia; short memory; cancer;  
KW sense or motor function; emotional reaction; fear response; panic;  
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;  
KW tranquiliser.  
XX  
OS Homo sapiens.  
XX  
PN EP1447413-A2.  
XX  
PD 18-AUG-2004.  
XX  
PF 12-FEB-2004; 2004EP-00003145.  
XX  
PR 14-FEB-2003; 2003JP-00102207.  
PR 09-MAY-2003; 2003JP-00131452.  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
XX  
DR WPI: 2004-583265/57.  
DR N-PSDB; ADR10442.  
XX  
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,  
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX  
PS Claim 1; SEQ ID NO 3987; 2686pp; English.  
XX



```
XX PD 18-JAN-2001.
XX XX
XX PF 06-JUL-2000; 2000WO-US018509.
XX XX
XX PR 07-JUL-1999; 99US-0142678P.
XX XX
XX PA (INCY-) INCYTE GENOMICS INC.
XX XX
XX PI Tang YT, Yue H;
XX XX
XX DR WPI; 2001-147193/15.
XX DR N-PSDB; AAF25338.
XX XX
XX PT New human detoxification protein and polynucleotide, useful for
XX PT diagnosis, prevention and treatment of autoimmune/inflammatory disorders
XX PT and cell proliferative disorders including cancer.
XX PS Claim 1; Page 77; 79pp; English.
XX XX
XX CC The present sequence represents a human detoxification polypeptide
XX CC (DETX). DETX and its (ant)agonists are useful for preventing or treating
XX CC disorders associated with decreased or increased expression or activity
XX CC of DETX. DETX polypeptides are useful for screening compounds that
XX CC specifically binds to DETX and for identifying (ant)agonists. Diseases
XX CC prevented, treated and diagnosed include cancers (e.g. leukaemia,
XX CC melanoma, adenocarcinoma, cancers of the brain, bone marrow, breast,
XX CC kidney, liver, pancreas, prostate and uterus), autoimmune/inflammatory
XX CC disorders (e.g. rheumatoid arthritis, asthma, atherosclerosis, autoimmune
XX CC thyroiditis, psoriasis and ulcerative colitis), bacterial, fungal,
XX CC parasitic infections and cell proliferative disorders (e.g. actinic
XX CC keratosis, arteriosclerosis, cirrhosis and hepatitis). Anti-DETX
XX CC antibodies may be used as antagonists, as a targeting or delivery
XX CC mechanism for bringing pharmaceutical agents into contact with cells or
XX CC tissues expressing DETX and for diagnosis of DETX-related disorders
XX SQ
SQ Sequence 234 AA;
Query Match 59.2%; Score 620.5; DB 4; Length 234;
Best Local Similarity 62.4%; Pred. No. 3.6e-60;
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;
QY 5 DLQDLP SATIACHLDP RVFDGLCR AKFESLFR TYDKDTTFQYFKSFRKVRINFSNPLSA 64
Db 42 DFNDLPNSLFA CNVHQSVFEGESKEKFEGLFR TYDDCVTFQLFKSFRVRINFSNPKSA 101
QY 65 ADARLRLHKT EFLGKEMKLYFAQT LHI GSS-----HLAPNDPKQFLISPSPAPPGVKOV 120
Db 102 ARARIELHETQFRGKKLKYFAQVQTPETDGDGKLHLAPPQPAKQFLISPSPAPPGWQPI 161
QY 121 EDATPVINYD LLYAISKLGPGK EYELHAATDPTPSVVHVCSDOENEEEMERMKRP 180
Db 162 NDATPVINYD LLYAVAKGPGKE YELHAGTESTPSVVHVCDSDIEEDDPK-----TSP 216
QY 181 KP KIIQTRRPEYTP 194
Db 217 KP KIIQTRRGLPP 230
RESULT 11
ADB64062
ID ADB64062 standard; protein; 243 AA.
XX ADB64062;
XX XX
XX DT 04-DEC-2003 (first entry)
XX XX
XX DE Human protein encoded by clone BRAWH20014590.
XX XX
XX KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
XX KW cell regeneration; membrane protein; signal transduction-related protein;
XX KW transcription-related protein; osteoporosis; neurological disease;
XX KW cancer; tumour.
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XX XX Homo sapiens.
XX OS
XX PN EP1308459-A2.
XX XX
XX PD 07-MAY-2003.
XX XX
XX PF 28-MAR-2002; 2002EP-00007401.
XX XX
XX PR 05-NOV-2001; 2001JP-00379298.
XX PR 25-JAN-2002; 2002US-00350978.
XX XX
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX XX
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX XX
XX DR WPI; 2003-450961/43.
XX DR N-PSDB; ADS62092.
XX XX
XX PT New polynucleotides and polypeptides, useful for developing a diagnostic
XX PT marker or medicines for regulation of their expression and activity, or
XX PT as targets of gene therapy.
XX XX
XX PS Claim 1; Page; 222pp; English.
XX XX
XX CC The invention discloses a polynucleotide comprising a sequence selected
XX CC from 1970 fully defined nucleotide sequences which encode novel
XX CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
XX CC or its partial peptide, an antibody binding to the polypeptide or peptide
XX CC of the polynucleotide, immunologically assaying the polypeptide or
XX CC peptide of the polynucleotide by contacting the polypeptide or peptide
XX CC with the antibody of the encoded protein, and observing the binding
XX CC between the two, a transformant carrying the polynucleotide in an
XX CC expressible manner and an antisense polynucleotide. The oligonucleotide
XX CC is useful as a primer for synthesising the polynucleotide, or as a probe
XX CC for detecting the polynucleotide. The polynucleotides and encoded
XX CC proteins are useful as pharmaceutical agents and many disease-related
XX CC genes may be included in them, for developing a diagnostic marker or
XX CC medicines for regulation of their expression and activity, or as targets
XX CC of gene therapy. The genes are involved in tissue and/or cell
XX CC regeneration. Membrane proteins, signal transduction-related proteins,
XX CC transcription-related proteins, disease-related proteins and genes
XX CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
XX CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
XX CC the activity or expression of the encoded protein to treat diseases. The
XX CC sequence presented is a protein of the invention. Note: Some of the
XX CC sequence data for this patent is not represented in the printed
XX CC specification, but is based on sequence information supplied by the
XX CC European Patent Office.
XX SQ
SQ Sequence 243 AA;
Query Match 59.2%; Score 620.5; DB 7; Length 243;
Best Local Similarity 62.4%; Pred. No. 3.8e-60;
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;
QY 5 DLQDLP SATIACHLDP RVFDGLCR AKFESLFR TYDKDTTFQYFKSFRKVRINFSNPLSA 64
Db 51 DFNDLPNSLFA CNVHQSVFEGESKEKFEGLFR TYDDCVTFQLFKSFRVRINFSNPKSA 110
QY 65 ADARLRLHKT EFLGKEMKLYFAQT LHI GSS-----HLAPNDPKQFLISPSPAPPGVKOV 120
Db 111 ARARIELHETQFRGKKLKYFAQVQTPETDGDGKLHLAPPQPAKQFLISPSPAPPGWQPI 170
QY 121 EDATPVINYD LLYAISKLGPGK EYELHAATDPTPSVVHVCSDOENEEEMERMKRP 180
Db 171 NDATPVINYD LLYAVAKGPGKE YELHAGTESTPSVVHVCDSDIEEDDPK-----TSP 225
QY 181 KP KIIQTRRPEYTP 194
|||||
```

Db	226	KPKIIQTRRPGLPP	239	
RESULT 12				
AAM50760				
ID	AAM50760	standard; protein; 255 AA.		
XX				
AC	AAM50760;			
XX				
DT	18-APR-2002	(first entry)		
XX				
DE	Human Down syndrome critical region 1-like 1 protein.			
XX				
KW	Down syndrome critical region 1-like 1; DSCR1L1 alpha; human;			
KW	Down syndrome; Alzheimer's disease; dementia; transgenic;			
KW	neuroprotective; nontropic; anticonvulsant; diagnosis; therapy.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Misc-difference 11	/note= "encoded by TNG"		
FT	Domain	129..199		
FT	Region	169..176		
FT		/note= "ISPPXSP box"		
XX	WO200204513-A2.			
XX				
PD	17-JAN-2002.			
XX				
PF	11-JUL-2001; 2001WO-US021982.			
XX				
PR	11-JUL-2000; 2000US-00614474.			
XX				
PA	(INCY-) INCYTE GENOMICS INC.			
XX				
PI	Loring JF, Tingley DW, Edwards CM, Streeter DG;			
XX				
DR	WPI; 2002-164633/21.			
DR	N-PSDB; ABA91457.			
XX				
PT	Novel Down syndrome critical region 1-like 1 protein and nucleic acid			
PT	encoding the protein useful for diagnosis and treatment of Alzheimer's			
PT	disease, Down syndrome and other forms of dementia.			
XX				
PS	Claim 1; Page 47-49; 54pp; English.			
XX				
CC	The present sequence is that of novel Down syndrome critical region 1-			
CC	like 1 protein (DSCR1L1 alpha). Northern analysis indicated expression of			
CC	DSCR1L1 alpha in various libraries, with the highest abundance in tissues			
CC	from the nervous system, including tissues associated with schizophrenia,			
CC	Huntington's disease, epilepsy and amyotrophic lateral sclerosis. An			
CC	absence of DSCR1L1 expression was observed in 7 of 8 libraries from			
CC	subjects with Alzheimer's disease. A claimed method for detecting			
CC	differential expression of a nucleic acid encoding DSCR1L1 alpha can be			
CC	used to diagnose Down syndrome, Alzheimer's disease and other forms of			
CC	dementia. The purified DSCR1L1 alpha protein, or a portion of it, can be			
CC	used to identify ligands which specifically bind the protein, such as a			
CC	DNA or RNA molecule, peptide nucleic acid, peptide, protein, mimetic,			
CC	agonist, antagonist, antibody, immunoglobulin inhibitor or drug, for use			
CC	as a therapeutic. The protein can also be used to raise antibodies useful			
CC	in diagnosis and therapy			
XX				
SQ	Sequence 255 AA;			
Query Match	59.2%;	Score 620.5;	DB 5;	Length 255;
Best Local Similarity	62.4%;	Pred. No. 4.1e-60;		
Matches 121;	Conservative 22;	Mismatches 42;	Indels 9;	Gaps 2;
OY	5	DIQDLPSATIAChLDPFRVFDGLCRAKFSLFRYDKDTTFQYFKSFRVRINFNSPLSA	64	
Db	63	DPNDLPNSLFACNVHQSVFEGESKEFGLFRYDCCVTFFQLFKSFRVRINFNSPKSA	122	

OY	65	ADARLRLHKTEFLGKEMKLYFAQTLLHIGSS----	HLAPPNDKQFLISPPASPPVGVKQV	120
Db	123	ARARIELHETQPRGKLLKLYFAQVTPETDGDGKHLAPPQAKQFLISPPSPVGVQPI	182	
OY	121	EDATPVINYDLIYALSKLPGCKEYELHAATDTPSVVVHVHVCSDQENEEEEEEMERMKP	180	
Db	183	NDATPVLYNLLYAVAKLPGCKEYELHAGTESTPSVVVVHVHVCSDIEEDDPK-----	TSP	237
OY	181	KPKIIQTRRPEYTP	194	
Db	238	KPKIIQTRRPGLPP	251	
RESULT 13				
ADE37339				
ID	ADE37339	standard; protein; 255 AA.		
XX				
AC	ADE37339;			
XX				
DT	29-JAN-2004	(first entry)		
XX				
DE	Human Down syndrome critical region 1-like 1alpha protein.			
XX				
KW	Down syndrome critical region 1-like 1alpha protein; nontropic;			
KW	neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;			
XX	human.			
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Misc-difference 11	/label= OTHER		
FT		/note= "OTHER= Unknown or other amino acid; encoded by		
FT		TNG"		
XX				
PN	US2003186333-A1.			
XX				
PD	02-OCT-2003.			
XX				
PF	06-NOV-2002; 2002US-00290438.			
XX				
PR	11-JUL-2000; 2000US-00614474.			
XX				
PA	(INCY-) INCYTE GENOMICS INC.			
XX				
PI	Loring JF, Tingley DW, Edwards CM, Streeter DG;			
XX				
DR	WPI; 2003-811734/76.			
DR	N-PSDB; ADE37338.			
XX				
PT	New purified Down syndrome critical region 1-like 1 protein, used for			
PT	diagnosing and treating Alzheimers disease, and for identifying and			
PT	purifying antibodies that specific bind to the protein.			
XX				
PS	Example 8; Fig 1; 39pp; English.			
XX				
CC	This invention relates to a novel purified Down syndrome critical region			
CC	1-like 1 protein comprising a polypeptide having fully defined sequence			
CC	of 255 amino acids, as given in the specification. Compounds which			
CC	modulate the protein of the invention may have nontropic or			
CC	neuroprotective activity. The protein sequence of the invention and the			
CC	CDNA sequence which encodes it may be useful for peptide therapy and gene			
CC	therapy respectively. The invention may prove useful in development of			
CC	therapeutics for the treatment of Alzheimer's disease. The present			
CC	sequence is the amino acid sequence of the human Down syndrome critical			
CC	region 1-like 1alpha protein of the invention. Note: This sequence is			
CC	given as Seq ID2 in the sequence listing but is referred to as Seq ID1			
CC	throughout the specification.			
XX				
SQ	Sequence 255 AA;			
Query Match	59.2%;	Score 620.5;	DB 7;	Length 255;



Best Local Similarity 62.4%; Pred. No. 4.1e-60;  
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

QY 5 DLQDLSATACHLDRVFDGLCRAKFESLFTYDKDTTFQYFKSKVRINFNSPLSA 64  
Db 63 DFNDLNSLFAACNVHVSFEGESKEKFEGLFTYDDCVTFQYFKSKVRINFNSPKSA 122  
QY 65 ADARLRLHTEFLGKEMKLYFAQTLHIGSS----HLAPPNDKQFLISPPASPPVGVKQV 120  
Db 123 ARARIELHETQFGKKLYFAQVOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWI 182  
QY 121 EDATPVINDLLVAISKLGEGKVELHAAATDPTSPVVHVCSQDNEEEEMERMRKP 180  
Db 183 NDATPVNLVNDLLYAVAKLGEGKVELHAGTSTPSVVHVCDSDIEBEDPK-----TSP 237  
QY 181 KPKIIOTRRPEYTP 194  
Db 238 KPKIIOTRRPGLPP 251

## RESULT 14

AAE18913  
ID AAE18913 standard; protein; 197 AA.

XX AAE18913;

XX 17-MAY-2002 (first entry)

XX Mouse MCIP associated proein #4.

XX Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
KW heart failure; cardiomyopathy; heart disease; mouse.

XX Mus musculus.

XX WO200204491-A2.

XX 17-JAN-2002.

XX 06-JUL-2001; 2001WO-US021662.

XX 07-JUL-2000; 2000US-0216601P.

XX 13-FEB-2001; 2001US-00782953.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (WILL/) WILLIAMS S R.

XX (ROTH/) ROTHERMEL B.

XX Williams SR, Rothermel B;

XX WPI; 2002-179698/23.

XX N-PSDB; AAD30154.

XX Screening for modulators of muscle calcineurin interacting protein (MCIP)  
PT binding, expression or phosphorylation, useful for treating cardiac  
PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a  
PT test compound.

XX Disclosure; Page 154; 174pp; English.

XX The invention relates to muscle calcineurin interacting proteins (MCIPs)  
XX and nucleic acid molecules encoding such proteins. MCIPs form a physical  
XX complex with the catalytic subunit of calcineurin and increased levels of  
XX MCIPs correspond to a reduced ability of calcineurin to stimulate  
XX transcription of certain target genes. The invention also relates to  
XX methods for identifying modulators of MCIP binding, expression or  
XX phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin  
XX may be used for treating cardiac hypertrophy and heart failure.  
XX Antibodies to MCIP can be used in characterizing the MCIP content of  
XX healthy and diseased tissues and subsequently for determining the  
XX presence or absence of cardiomyopathy or as predictor of heart disease.  
XX The present sequence is mouse MCIP associated protein. Note: This  
XX sequence has been described as mouse MCIP2 encoding DNA in the

CC specification, however the sequence seems to be a MCIP associated protein  
XX  
SQ Sequence 197 AA;

Query Match 58.5%; Score 613.5; DB 5; Length 197;

Best Local Similarity 63.3%; Pred. No. 1.7e-59;

Matches 119; Conservative 22; Mismatches 38; Indels 9; Gaps 2;

QY 11 SATIACHLDRPVFDGLCRAKFESLFTYDKDTTFQYFKSKVRINFNSPLSAADARLR 70

Db 11 STLAVCVDFVFTNQEVKEKFEGLFTYDDCVTFQYFKSKVRINFNSPKSAARARIE 70

QY 71 LHKTEFLGKEMKLYFAQTLHIGSS----HLAPPNDKQFLISPPASPPVGVKQVDPV 126

Db 71 LHETQFRGKKLYFAQVOTPETDGDKLHLAPPQAKQFLISPPSPVGVKQVDPV 130

QY 127 INYDLLYAIKLGEGKVELHAAATDPTSPVVHVCSQDNEEEEMERMRKPKKIIQ 186

Db 131 LNYDLLYAVAKLGEGKVELHAGTSTPSVVHVCDSDMEBEDPK-----TSPKPKIIQ 185

QY 187 TRRPEYTP 194

Db 186 TRRPGGLPP 193

## RESULT 15

ABO07172

ID ABO07172 standard; protein; 197 AA.

XX ABO07172;

XX 13-AUG-2003 (first entry)

XX Human p53 modifying protein, SEQ ID 132.

XX Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;  
KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;  
KW lung cancer; ovarian cancer; angiogenesis; cell cycle;  
KW apoptotic disorder; cell proliferation disorder.

XX Homo sapiens.

XX WO2002099122-A1.

XX 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US017382.

XX 05-JUN-2001; 2001US-0296076P.

XX 10-OCT-2001; 2001US-0328605P.

XX 15-FEB-2002; 2002US-0357253P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX WPI; 2003-156859/15.

XX N-PSDB; ACD13348.

XX Identifying modulators of the p53 pathway for use in treating apoptotic  
PT or cell proliferation disorders, comprises screening for agents that  
PT modulate activity of a human ortholog of genes that modify the p53  
PT pathway in Drosophila.

XX Example 2; Page 434-435; 678pp; English.

XX The invention relates to identifying (M1) a candidate p53 pathway  
CC modulating agent, by contacting an assay system comprising a purified HM  
CC polypeptide (human orthologue of genes that modify the p53 pathway in  
CC Drosophila) or nucleic acid with a test agent under conditions, where but  
CC for the presence of the test agent, the system provides a reference  
CC activity, and detecting a test agent-biased activity of the assay system.  
CC Also included are modulating (M2) a p53 pathway of a cell (comprising



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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:55 ; Search time 27 Seconds  
(without alignments)  
547.426 Million cell updates/sec

Title: US-09-575-580B-4  
Perfect score: 1048  
Sequence: 1 MEEVDLQDLPSTAIACHLDP.....RPKPKIIQTRRPEYTPHLS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/6C\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	847.5	80.9	171	4 US-09-949-016-6493	Sequence 6493, Ap
2	847.5	80.9	173	4 US-09-949-016-11053	Sequence 11053, A
3	835.5	79.7	171	2 US-08-665-040-2	Sequence 2, Appli
4	620.5	59.2	255	4 US-09-614-474-2	Sequence 2, Appli
5	609.5	58.2	206	4 US-09-949-016-11450	Sequence 11450, A
6	596.5	56.9	192	4 US-09-614-474-10	Sequence 10, Appl
7	596.5	56.9	192	4 US-09-949-016-6659	Sequence 6659, Ap
8	596	56.9	241	4 US-09-614-474-11	Sequence 11, Appl
9	596	56.9	248	4 US-09-949-016-7081	Sequence 7081, Ap
10	439	41.9	111	4 US-09-513-999C-5949	Sequence 5849, Ap
11	372.5	35.5	289	4 US-09-270-767-44503	Sequence 44503, A
12	90.5	8.6	4019	4 US-09-854-133-425	Sequence 425, App
13	88	8.4	284	5 PCT-US94-09752-4	Sequence 4, Appli
14	86.5	8.3	822	4 US-09-824-734-3	Sequence 3, Appli
15	84.5	8.1	719	4 US-09-641-741-28	Sequence 28, Appl
16	83	7.9	367	4 US-09-248-796A-15492	Sequence 15492, A
17	82	7.8	1128	4 US-09-641-741-30	Sequence 30, Appl
18	82	7.8	1128	4 US-09-060-482-8	Sequence 8, Appli
19	81	7.7	1128	1 US-08-111-539-2	Sequence 2, Appli
20	80	7.6	314	4 US-09-328-352-5324	Sequence 5324, Ap
21	80	7.6	492	4 US-09-792-024-91	Sequence 91, Appl
22	79	7.5	708	4 US-09-949-016-7574	Sequence 7574, Ap
23	79	7.5	1132	1 US-08-446-038B-18	Sequence 18, Appl
24	79	7.5	1132	1 US-08-446-010B-18	Sequence 18, Appl
25	79	7.5	1132	2 US-08-805-445-18	Sequence 18, Appl
26	79	7.5	1132	2 US-08-064-067D-18	Sequence 18, Appl
27	79	7.5	1132	2 US-09-066-208-18	Sequence 18, Appl

28	79	7.5	1142	1 US-08-097-997A-11	Sequence 11, Appl
29	79	7.5	1142	3 US-08-665-574C-11	Sequence 11, Appl
30	79	7.5	1142	3 US-08-946-994-11	Sequence 11, Appl
31	79	7.5	1154	1 US-08-357-598-7	Sequence 7, Appli
32	79	7.5	1154	1 US-08-446-010B-24	Sequence 24, Appl
33	79	7.5	1154	2 US-09-003-289-7	Sequence 7, Appli
34	79	7.5	1154	4 US-09-963-137-203	Sequence 203, App
35	79	7.5	1154	5 PCT-US95-16435-7	Sequence 7, Appli
36	78.5	7.5	547	4 US-09-877-730-26	Sequence 26, Appl
37	78.5	7.5	624	4 US-09-877-730-24	Sequence 24, Appl
38	78.5	7.5	628	4 US-09-877-730-30	Sequence 30, Appl
39	78.5	7.5	712	4 US-09-877-730-22	Sequence 22, Appl
40	78.5	7.5	793	4 US-09-877-730-28	Sequence 28, Appl
41	78.5	7.5	826	4 US-09-877-730-16	Sequence 16, Appl
42	78.5	7.5	864	4 US-09-883-096-2	Sequence 2, Appli
43	78.5	7.5	904	4 US-09-877-730-6	Sequence 6, Appli
44	78.5	7.5	907	4 US-09-877-730-20	Sequence 20, Appl
45	78.5	7.5	985	4 US-09-877-730-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-6493  
; Sequence 6493, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6493  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6493

Query Match	80.9%	Score	847.5	DB	4	Length	171
Best Local Similarity	95.9%	Pred. No.	7.8e-90				
Matches	162	Conservative	3	Mismatches	3	Indels	1
Gaps	1						
QY	30	AKFESLFRTYDXTTFQYFKSKFRVIRNFSNPLSADARLRLHKTFLGKMKLYFAQTL	89				
Db	4	AKFESLFRTYDXTTFQYFKSKFRVIRNFSNPLSADARLRLHKTFLGKMKLYFAQTL	63				
QY	90	HGSSHLAPPNDKOFLLSPASPVPVGWKQVDATPVINDLLYATSKLGPGEKVELHAA	149				
Db	64	HGSSHLAPPNDKOFLLSPASPVPVGWKQVDATPVINDLLYATSKLGPGEKVELHAA	123				
QY	150	TDPTSVVVHVHVCESQENEEEEEMRMKRPKPKIIQTRRPEYTPHLS	198				
Db	124	TDPTSVVVHVHVCESQENEEEEEMRMKRPKPKIIQTRRPEYTPHLS	171				

RESULT 2

US-09-949-016-11053  
; Sequence 11053, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF



Db 238 KPQIIQTRRPLGP 251

RESULT 5

US-09-949-016-11450

; Sequence 11450, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11450

; LENGTH: 206

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-11450

Query Match 58.2%; Score 609.5; DB 4; Length 206;

Best Local Similarity 63.3%; Pred. No. 3.4e-62;

Matches 119; Conservative 21; Mismatches 39; Indels 9; Gaps 2;

QY 11 SATIACHLDPRVFDGLCRKAFESLRTYDQDTTFOYFKSKFRVRINFSNPLSAADARLR 70

Db 20 SILVACVDVEVFTNQEVKEFGGLFRTYDDCVTFQLFKSKFRVRINFSNPKSAARARIE 79

QY 71 LHKTEFLGKEMKLYFAQTLHIGSS----HLAPPNDPKQLISPPASPPVGVKQVEDATPV 126

Db 80 LHETQFRGKKLYFAQVQTPETDGDGKLHAPPQPAKQFLISPPSSPPVQWQPIINDATPV 139

QY 127 INYDLYAISKLGPGEKYLHAATDTPSVVHVCSDOENEEEMERMKRKPQKIIQ 186

Db 140 LNYDLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDIEEDDPK-----TSPKPKIIQ 194

QY 187 TRPEYTP 194

Db 195 TRAPGLPP 202

RESULT 6

US-09-614-474-10

; Sequence 10, Application US/09614474

; Patent No. 6524819

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.

; APPLICANT: Tingley, Debra W.

; APPLICANT: Edwards, Carla M.

; APPLICANT: Streeter, David G.

; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS

; FILE REFERENCE: PC-0013 US

; CURRENT APPLICATION NUMBER: US/09/614,474

; CURRENT FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PERL Program

; SEQ ID NO 10

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6524819 gl435040

US-09-614-474-10

Query Match 56.9%; Score 596.5; DB 4; Length 192;

Best Local Similarity 62.2%; Pred. No. 9.8e-61;

Matches 117; Conservative 21; Mismatches 41; Indels 9; Gaps 2;

QY 11 SATIACHLDPRVFDGLCRKAFESLRTYDQDTTFOYFKSKFRVRINFSNPLSAADARLR 70

Db 6 STLVACVDVEVFTNQEVKEFGGLFRTYDDCVTFQLFKSKFRVRINFSNPKSAARARIE 65

QY 71 LHKTEFLGKEMKLYFAQTLHIGSS----HLAPPNDPKQLISPPASPPVGVKQVEDATPV 126

Db 66 LHETQFRGKKLYFAQVQTPETDGDGKLHAPPQPAKQFLISPPSSPPVQWQPIINDATPV 125

QY 127 INYDLYAISKLGPGEKYLHAATDTPSVVHVCSDOENEEEMERMKRKPQKIIQ 186

Db 126 LNYDLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDIEEDDPK-----TSPKPKIIQ 180

QY 187 TRPEYTP 194

Db 181 TRRPLGP 188

RESULT 7

US-09-949-016-6659

; Sequence 6659, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6659

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6659

Query Match 56.9%; Score 596.5; DB 4; Length 192;

Best Local Similarity 62.2%; Pred. No. 9.8e-61;

Matches 117; Conservative 21; Mismatches 41; Indels 9; Gaps 2;

QY 11 SATIACHLDPRVFDGLCRKAFESLRTYDQDTTFOYFKSKFRVRINFSNPLSAADARLR 70

Db 6 STLVACVDVEVFTNQEVKEFGGLFRTYDDCVTFQLFKSKFRVRINFSNPKSAARARIE 65

QY 71 LHKTEFLGKEMKLYFAQTLHIGSS----HLAPPNDPKQLISPPASPPVGVKQVEDATPV 126

Db 66 LHETQFRGKKLYFAQVQTPETDGDGKLHAPPQPAKQFLISPPSSPPVQWQPIINDATPV 125

QY 127 INYDLYAISKLGPGEKYLHAATDTPSVVHVCSDOENEEEMERMKRKPQKIIQ 186

Db 126 LNYDLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDIEEDDPK-----TSPKPKIIQ 180

QY 187 TRPEYTP 194

Db 181 TRRPLGP 188

RESULT 8

US-09-614-474-11

; Sequence 11, Application US/09614474

; Patent No. 6524819

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.

```
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6524819 g6017919
US-09-614-474-11

Query Match          56.9%; Score 596; DB 4; Length 241;
Best Local Similarity 61.9%; Pred. No. 1.6e-60;
Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY      2  EVDVQLDPSATIAACHLDRPVFDGLCRAKFESLFRITYDKDTTFQYFKSFKEVRINFSP 61
Db      38  EMDVLSDLTSLFACSVHAEVFEAREQKRFELFTYDDQVTFQYFKSFRVRINFSP 97

QY      62  LSAADARLRLHKTEFLGKEMKLYFAQTLHIG----SSHLAPPNDPKQFLISPPAPVGM 117
Db      98  EAAARARIELHETDFNGQKLYFAQVQMSGEVRDKSYLLPPQPVKQFLISPPAPVGM 157

QY      118  QVEDATPVINYDLYAISKLGPGKEYELHAATDTPSPVVHVCSDDQNEEEEMERM 177
Db      158  QKSEDAMPVINYDLLCAVSKLGPGKEYELHAGTESTPSVVHVCSSETEEEEE-----T 211

QY      178  KRPKKIIOTRRPE 191
Db      212  KNPKQKIAQTRRPD 225

RESULT 9
US-09-949-016-7081
; Sequence 7081, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7081
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7081

Query Match          56.9%; Score 596; DB 4; Length 248;
Best Local Similarity 61.9%; Pred. No. 1.6e-60;
Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY      2  EVDVQLDPSATIAACHLDRPVFDGLCRAKFESLFRITYDKDTTFQYFKSFRVRINFSP 61
Db      45  EMDVLSDLTSLFACSVHAEVFEAREQKRFELFTYDDQVTFQYFKSFRVRINFSP 104

QY      62  LSAADARLRLHKTEFLGKEMKLYFAQTLHIG----SSHLAPPNDPKQFLISPPAPVGM 117

; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6524819 g6017919
US-09-614-474-11

Query Match          56.9%; Score 596; DB 4; Length 241;
Best Local Similarity 61.9%; Pred. No. 1.6e-60;
Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY      2  EVDVQLDPSATIAACHLDRPVFDGLCRAKFESLFRITYDKDTTFQYFKSFKEVRINFSP 61
Db      38  EMDVLSDLTSLFACSVHAEVFEAREQKRFELFTYDDQVTFQYFKSFRVRINFSP 97

QY      62  LSAADARLRLHKTEFLGKEMKLYFAQTLHIG----SSHLAPPNDPKQFLISPPAPVGM 117
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QY      118  QVEDATPVINYDLYAISKLGPGKEYELHAATDTPSPVVHVCSDDQNEEEEMERM 177
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QY      178  KRPKKIIOTRRPE 191
Db      212  KNPKQKIAQTRRPD 225

RESULT 10
US-09-513-999C-5849
; Sequence 5849, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5849
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5849

Query Match          41.9%; Score 439; DB 4; Length 111;
Best Local Similarity 84.2%; Pred. No. 7.2e-43;
Matches 85; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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Db      11  SSLIACVANSDFSESETRAKFESLFRITYDKDTTFQYFKSFRVRINFSPNPLSAADARLR 70

QY      71  LHKTEFLGKEMKLYFAQTLHIGSSHLAPPNDPKQFLISPPA 111
Db      71  LHKTEFLGKEMKLYFAQTLHIGSSHLAPPNDPKQFLISPPA 111

RESULT 11
US-09-270-767-44503
; Sequence 44503, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44503
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44503

Query Match          35.5%; Score 372.5; DB 4; Length 289;
Best Local Similarity 43.8%; Pred. No. 1.4e-34;
Matches 71; Conservative 38; Mismatches 48; Indels 5; Gaps 3;

QY      3  EVD---LQDLPSATIAACHLDRPVFDGLCRAKFESLFRITYDKDTTFQYFKSFRVRINFSP 59
Db      111  EVDADSPDDLFTSLIVNIHSEVFANPELKHAMELFTFSESATFQWLRSFRRLRVNYD 170
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RESULT 13  
PCT-US94-09752-4  
; Sequence 4, Application PC/TUS9409752  
; GENERAL INFORMATION:  
; APPLICANT: David S. Strayer and Avinaesh Chander  
; TITLE OF INVENTION: Compositions and Methods for  
; TARGETING CELLS AND MODULATING PULMONARY SURFACTANT SECRETION  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jane Massey Licata, Esq.  
; STREET: 210 Lake Drive East, Suite 201  
; CITY: Cherry Hill  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb  
; MEDIUM TYPE: STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/09752  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/176,218

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RESULT 15
US-09-641-741-28
; Sequence 28, Application US/09641741
; Patent No. 6420155
; GENERAL INFORMATION:
; APPLICANT: Kerry E. Quinn
; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; TITLE OF INVENTION: encoding Same
; FILE REFERENCE: 15966-581
; CURRENT APPLICATION NUMBER: US/09/641,741
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-641-741-28

Query Match      8.1%; Score 84.5; DB 4; Length 719;
Best Local Similarity 21.8%; Pred. No. 1.1;
Matches 31; Conservative 27; Mismatches 37; Indels 47; Gaps 7;

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Db 585 LAVDPSRPWTQQRRMQRRQLQVRLRMREQRL---RRLNSTAGPATSPTP----ALMEPP 637
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
QY 111 ASP-----PVGWK--QVEDATPVINVDLLYAIKSLGPGKGYELHAATDPT 153
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 638 PSFTPAITLRPWELVLTPTTTAGWEESETETYTEVVT-----EFETEGTD-- 681
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QY 154 PSVVHVHCESDOENEEEEE 175
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Search completed: November 16, 2005, 16:31:56  
Job time : 29 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:57 ; Search time 100.8 Seconds  
(without alignments)  
821.875 Million cell updates/sec

Title: US-09-575-580B-4  
Perfect score: 1048  
Sequence: 1 MEEVDLQDLPSTACHLDP.....RPKPKIOTRRPEYTPHLS 198

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1048	100.0	198	9	US-09-782-953-3 Sequence 3, Appli
2	1048	100.0	198	9	US-09-782-953-4 Sequence 4, Appli
3	1002.5	95.7	197	9	US-09-782-953-15 Sequence 15, Appl
4	1002.5	95.7	197	9	US-09-782-953-16 Sequence 16, Appl
5	1002.5	95.7	197	16	US-10-755-889-120 Sequence 120, App
6	1002.5	95.7	252	15	US-10-104-047-2892 Sequence 2892, Ap
7	920.5	87.8	198	9	US-09-782-953-6 Sequence 6, Appli
8	920.5	87.8	198	9	US-09-782-953-7 Sequence 7, Appli
9	872.5	83.3	197	9	US-09-782-953-12 Sequence 12, Appl
10	872.5	83.3	197	9	US-09-782-953-13 Sequence 13, Appl
11	872.5	83.3	197	14	US-10-247-671-174 Sequence 174, App

12	847.5	80.9	171	15	US-10-428-487-24	Sequence 24, Appl
13	620.5	59.2	243	15	US-10-104-047-2216	Sequence 2216, Ap
14	620.5	59.2	255	14	US-10-290-438-2	Sequence 2, Appli
15	613.5	58.5	197	9	US-09-782-953-9	Sequence 9, Appli
16	613.5	58.5	197	9	US-09-782-953-10	Sequence 10, Appl
17	596.5	56.9	192	9	US-09-782-953-18	Sequence 18, Appl
18	596.5	56.9	192	9	US-09-782-953-19	Sequence 19, Appl
19	596.5	56.9	192	14	US-10-290-438-10	Sequence 10, Appl
20	596.5	56.9	197	18	US-10-764-425-126	Sequence 126, App
21	596	56.9	241	9	US-09-782-953-21	Sequence 21, Appl
22	596	56.9	241	9	US-09-782-953-22	Sequence 22, Appl
23	596	56.9	241	14	US-10-290-438-11	Sequence 11, Appl
24	595	56.8	212	9	US-09-782-953-24	Sequence 24, Appl
25	595	56.8	212	9	US-09-782-953-25	Sequence 25, Appl
26	497	47.4	142	9	US-09-925-302-790	Sequence 790, App
27	497	47.4	142	10	US-09-925-302-790	Sequence 790, App
28	379.5	36.2	292	20	US-11-097-143-41193	Sequence 41193, A
29	284	27.1	58	9	US-09-864-761-35379	Sequence 35379, A
30	284	27.1	58	9	US-09-864-761-43076	Sequence 43076, A
31	271.5	25.9	56	9	US-09-864-761-34111	Sequence 34111, A
32	136.5	13.0	32	14	US-10-194-155-8	Sequence 8, Appli
33	94	9.0	699	16	US-10-437-963-186586	Sequence 186586,
34	93	8.9	227	16	US-10-437-963-196664	Sequence 196664,
35	92	8.8	513	15	US-10-282-122A-48629	Sequence 48629, A
36	92	8.8	1455	18	US-10-511-698-114	Sequence 114, App
37	90.5	8.6	4019	9	US-09-738-973-425	Sequence 425, App
38	90.5	8.6	4019	9	US-09-854-133-425	Sequence 425, App
39	90.5	8.6	4019	14	US-10-144-649A-425	Sequence 425, App
40	89.5	8.5	915	15	US-10-276-774-2443	Sequence 2443, Ap
41	87.5	8.3	1477	20	US-11-097-143-12672	Sequence 12672, A
42	86.5	8.3	822	9	US-09-824-734-3	Sequence 3, Appli
43	86.5	8.3	822	16	US-10-749-386-3	Sequence 3, Appli
44	86	8.2	915	16	US-10-437-963-132441	Sequence 132441,
45	85	8.1	2816	15	US-10-240-145-145	Sequence 145, App

ALIGNMENTS

RESULT 1  
US-09-782-953-3  
; Sequence 3, Application US/09782953  
; Patent No. US20020150953A1  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, R. SANDERS  
; APPLICANT: ROTHERMEL, BEVERLY  
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)  
; FILE REFERENCE: UTSD:674P21  
; CURRENT APPLICATION NUMBER: US/09/782,953  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/216,601  
; PRIOR FILING DATE: 2000-07-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-782-953-3

Query Match	100.0%	Score 1048;	DB 9;	Length 198;
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Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	61	PLSAADARLRLHKTFLKEMKLYFAQTUHGSSHLAPPNDPKQFLISPPASPPVGWKQV	120	

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RESULT 2
US-09-782-953-4
; Sequence 4, Application US/09782953
; Patent NO. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674PE21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-4

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Query Match	100.08;	Score 1048;	DB 9;	Length 198;
Best Local Similarity	100.08;	Prod. No. 9.9e-97;		
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Db	1	MEEVDQLDPLSATIACHLDPRVFDGLCKRAKFESLFRTYDKDPTTFQYFKSKFVRINFSN	60	
Qy	61	PLSAADARLRHLKTEFLGKEMKLYFAQTLHTLGSSHLAPPNDPKQLISPPASPPVGMKQV	120	
Db	61	PLSAADARLRHLKTEFLGKEMKLYFAQTLHTLGSSHLAPPNDPKQLISPPASPPVGMKQV	120	
Qy	121	EDATPVNIDLLYIAISLKGPEKVELHAATDPTPSVVHVHCSDQENEEEEEMRMKRP	180	
Db	121	EDATPVNIDLLYIAISLKGPEKVELHAATDPTPSVVHVHCSDQENEEEEEMRMKRP	180	
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RESULT 3  
 US-09-782-953-15  
 ; Sequence 15, Application US/09782953  
 ; Patent No. US20020150953A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILLIAMS, R. SANDERS  
 ; APPLICANT: ROTHERMEL, BEVERLY  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
 ; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)  
 ; FILE REFERENCE: UTSD:674PZ1  
 ; CURRENT APPLICATION NUMBER: US/09/782,953  
 ; CURRENT FILING DATE: 2001-02-13  
 ; PRIOR APPLICATION NUMBER: 60/216,601  
 ; PRIOR FILING DATE: 2000-07-07  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 15  
 ; LENGTH: 197  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-782-953-15

	Query March	95.7%;	Score 1002.5;	DB 9;	Length 197;
	Best Local Similarity	96.5%;	Prod. No. 3.6e-92;		
	Matches 191;	Conservative	3;	Mismatches 3;	Indels 1; Gaps 1
Qy	1	MEEVDLDLP	SATTACHLDPRVFVDGL	CRAKFESLFRTYDKDTFYQYFKSFKRVINFSN	60
Db	1	MEEVDLDLP	SATTACHLDPRVFVDGL	CRAKFESLFRTYDKDTFYQYFKSFKRVINFSN	60
Qy	61	PLSAADARL	LHKTEFTLGKMKLYPAQTLH	TGSSHLAPPNDPKQLISPPASPVPVGWQV	120
Db	61	PFSAADARL	QLHKTEFTLGKMKLYPAQTLH	TGSSHLAPPNDPKQLISPPASPVPVGWQV	120
Qy	121	EDATPVN	LDLLYAI	SKLGPEKYEYELHAATDPTPSVVHVHVCESDOENEEBEEEMRMKRP	180
Db	121	EDATPVN	LDLLYAI	SKLGPEKYEYELHAATDPTPSVVHVHVCESDOE-KEEBEEMRMKRP	179
Qy	181	KPKIIQTRR	RPYTPPIHLS	198	
Db	180	KPKIIQTRR	RPYTPPIHLS	197	

```

RESULT 4
US-09-782-953-16
; Sequence 16, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674PZ1
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-16

```

RESULT 5  
US-10-755-889-120  
Sequence 120, Application US10755889  
Publication No. US20040171823A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: POLYNUCLEOTIDES AND  
TITLE OF INVENTION: PATHWAY

```

; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-120

Query Match          95.7%;   Score 1002.5;   DB 16;   Length 197;
Best Local Similarity 96.5%;   Pred No. 36e-92;
Matches 191;   Conservative 3;   Mismatches 3;   Indels 1;   Gaps 1

Qy 1 MEEVDQLPSATIACHLDPRVFVDGLCRAKFESLRTYDKDITTFQYFKSKRVRINF 60
Db 1 MEEVDQLPSATIACHLDPRVFVDGLCRAKFESLRTYDKDITTFQYFKSKRVRINF 60

Qy 61 PLSAADARLRHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWQV 120
Db 61 PFSAADARLRQHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWQV 120

Qy 121 EDATPVNIDLLYAIKSLGPGKEKVELHAATDTPSVVHVHCSDOENEEEMERMKRP 180
Db 121 EDATPVNIDLLYAIKSLGPGKEKVELHAATDTPSVVHVHCSDQE-KBEEEMERMRRP 179

Qy 181 KPKIQTRRPEYTPIHLS 198
Db 180 KPKIQTRRPEYTPIHLS 197

RESULT 6
US-10-104-047-2892
; Sequence 2892, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2892
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2892

Query Match          95.7%;   Score 1002.5;   DB 15;   Length 252;
Best Local Similarity 96.5%;   Pred: No. 5e-92;
Matches 191;   Conservative 3;   Mismatches 3;   Indels 1;   Gaps 1

Qy 1 MEEVDQLPSATIACHLDPRVFVDGLCRAKFESLRTYDKDITTFQYFKSKRVRINF 60
Db 56 MEEVDQLPSATIACHLDPRVFVDGLCRAKFESLRTYDKDITTFQYFKSKRVRINF 115

Qy 61 PLSAADARLRHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWQV 120
Db 116 PFSAADARLRQHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWQV 175

Qy 121 EDATPVNIDLLYAIKSLGPGKEKVELHAATDTPSVVHVHCSDOENEEEMERMKRP 180
Db 176 EDATPVNIDLLYAIKSLGPGKEKVELHAATDTPSVVHVHCSDQE-KBEEEMERMRRP 234

Qy 181 KPKIQTRRPEYTPIHLS 198

```

Qy	4	VDLODLP---SATTACHLDPRVFDUGLCRAKFESLFRYTDKDTTQYFKSFKRVIRNFSN	60
Db	1	MDFRDFSYNFSSLIACVANDVDVSESETRAKFESLFRTYTDKDTTQYFKSFKRVIRNFSN	60
Qy	61	PLSAAADARLRLLHKTEFLGKMKLYFAQTLHTGSSHLAPPNDPKQFI.SPPASPPVGVKQV	120
Db	61	PLSAAADARLRLLHKTEFLGKMKLYFAQTLHTGSSHLAPPNDPKQFI.SPPASPPVGVKQV	120
Qy	121	EDATPVINYDLLYIAISKLGPGKEYELHAATDTPPSVVHVVCESDQENEEEEEMERMKRP	180
Db	121	EDATPVINYDLLYIAISKLGPGKEYELHAATDTPPSVVHVVCESDQENEEEEEMERMKRP	180
Qy	181	KPKIIQTRRPBYTPHLS	198
Db	181	KPKIIQTRRPBYTPHLS	198





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:43:46 ; Search time 12.15 Seconds  
(without alignments)  
1567.977 Million cell updates/sec

Title: US-09-575-580B-4

Perfect score: 1048

Sequence: 1 MEEVDLQDLPSATIACHLDP.....RPKPKLIQRRPEYTPIHLS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	355	33.9	239	T34305	hypothetical prote
2	139.5	13.3	315	T49641	nebula related pro
3	95.5	9.1	163	S62444	conserved hypothet
4	94	9.0	318	C84651	hypothetical prote
5	92	8.8	992	T46337	hypothetical prote
6	91.5	8.7	1274	D84485	probable retroelem
7	88	8.4	284	B48316	surfactant protein
8	88	8.4	630	S29796	hypothetical prote
9	88	8.4	721	S29795	hypothetical prote
10	86.5	8.3	822	S30198	Na+/H+-exchanging
11	86	8.2	338	S73902	UDP-glucose 4-epim
12	84.5	8.1	719	S51739	transcription repr
13	83	7.9	561	JC2436	5'-nucleotidase [E
14	83	7.9	1173	T31421	C-terminal domain-
15	82	7.8	697	E96752	hypothetical prote
16	82	7.8	1477	T13797	tumor suppressor pr
17	81.5	7.8	528	C69323	conserved hypothet
18	81	7.7	151	T10768	latex allergen Hev
19	80.5	7.7	280	C64471	hypothetical prote
20	80.5	7.7	360	S12850	protein TPX - Ther
21	80	7.6	681	T17342	hypothetical prote
22	79.5	7.6	797	A70453	glutamate ammonia
23	79.5	7.6	904	I38757	homolog of Drosoph
24	79.5	7.6	926	I38756	hypothetical prote
25	79.5	7.6	1020	B86414	hypothetical prote
26	79.5	7.6	1136	T26953	hypothetical prote
27	79.5	7.6	1146	C83304	hypothetical prote
28	79.5	7.6	1557	T29132	hypothetical prote
29	79	7.5	684	F85075	hypothetical prote

30	79	7.5	1154	2	A39577	protein-tyrosine k
31	79	7.5	1216	2	T09224	spindle assembly c
32	79	7.5	13055	2	T16580	hypothetical prote
33	78.5	7.5	211	2	S37792	hypothetical prote
34	78.5	7.5	290	2	T42526	hypothetical prote
35	78.5	7.5	1706	2	I84499	zinc finger protei
36	78.5	7.5	1880	2	T18531	tractin - medicina
37	78	7.4	454	2	AE1244	acetyl-CoA coxsy
38	78	7.4	467	1	A49377	involucrin - mouse
39	78	7.4	677	2	T00369	hypothetical prote
40	77.5	7.4	441	2	A86151	hypothetical prote
41	77.5	7.4	455	2	B86427	hypothetical prote
42	77.5	7.4	621	2	T15929	hypothetical prote
43	77.5	7.4	627	2	A41609	dnak-type molecula
44	77.5	7.4	1211	2	T42230	AF4 protein - mous
45	77	7.3	340	2	B84771	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

T34305

hypothetical protein F54E7.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T34305

R:Bentley, D.

submitted to the EMBL Data Library, June 1994

A:Description: The sequence of C. elegans cosmid F54E7.

A:Reference number: Z21502

A:Accession: T34305

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-239 <BEN>

A:Cross-references: UNIPROT:P53806; EMBL:U00067; PIDN:AAC77519.1; GSPDB:GN00021; CESP:F

A:Experimental source: strain Bristol N2; clone F54E7

C:Genetics:

A:Gene: CESP:F54E7.7

A:Map position: 3

A:Introns: 40/3; 78/2; 165/2; 205/1

Query Match	33.9%	Score 355;	DB 2;	Length 239;
Best Local Similarity	41.0%;	Pred. No. 3.9e-24;		
Matches 75;	Conservative 36;	Mismatches 68;	Indels 4;	Gaps 3
QY	8	DLPSATIACHLDP	RVFVDGLCRAPESL	FTYDKDTTFQYFKSFKRVRINFSNPLSAADA 67
Db	27	DLPNAIIVTQVPED	VFDNKKANFSSLF	TQIEKDIHDFLRSFRRVRVIFSSPENATAA 86
QY	68	RLRLHKTEFLGEMKLY	FAQTLLHI--GSSHLAPP	PPDKQFLISPPASPPVGNKQVEDATP 125
Db	87	KLIQVGFSGKHELKAF	FAQRIYMSANSQMLSP	PLEKQFLISPPCSPPVGMETKOMPP 146
QY	126	VT--NYDLLVAISK	LGPEKYEYELHAATD	TPSVVHVCSDDQNEEEEEEMRMKRPKPI 184
Db	147	VVCNFDLMARLAS	FAIDEXYEVHNGDELT	PAIIVHPCETPID-VPSAIEMPTRPSPSS 205

##### RESULT 2

T49641

nebula related protein [imported] - Neurospora crassa

N:Alternate names: protein B5022.230

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C:Accession: T49641

R:Schulte, U.; Aign, V.; Hohaisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura  
submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022





Db 301 EQAPSPAAACEKQHQHQAELGPGQEAEDPEEKVAVSPTPPVSPVSTPVPAPPEQ 360  
QY 157 -----VVHYCESDQNEEEEMERMKRPKPKIOTRRPEYTPIH 196  
Db 361 LSEALKAMEEAAVQVLEQDORHLLSKQ-EKKQQLREKLQCQEESEILRLH 411  
RESULT 6  
D84485  
probable retroelement pol polyprotein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: D84485  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: D84485  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-1274 <STO>  
A;Cross-references: UNIPROT:Q9ZQK2; GB:AE002093; NID:94309763; PIDN:AAD15532.1; GSPDB:GN  
C:Genetics:  
A;Gene: At2g07400  
A;Map position: 2

Query Match 8.7%; Score 91.5; DB 2; Length 1274;  
Best Local Similarity 23.1%; Pred. No. 7.8;  
Matches 51; Conservative 30; Mismatches 83; Indels 51; Gaps 9;  
QY 24 VDGLCRAKFESLFRDYDKDTTFQYFKSKRVIRNFNSNPLSAADAR-LRLHKTFLGKE-- 80  
Db 673 IESRVAKTEGREGSTENDV-----KQIKELKAIADSKSSVIRDMYLAKTQPQTQDN 727  
QY 81 MKLYFAQTLLHI-----GSSHLAPPND-----KQFLISPPA-----SPVGVWK 118  
Db 728 PKVOTQOTPDVPKPTNNQFATSPPPSKQADVCKEKTINELIQPPGRGRKPSQPK 787  
QY 119 QVEDATPVNYDLLYAIKLGPEKYEHLA-----ATDTPSPVVHVHVCSDQNEEEEEE 173  
Db 788 KVSPTMPKTI-----TIKKLPKQEAKEABEDSDVDVDTDKVVSYNEMLPESDDEEE 841  
QY 174 MERMKRPKPKIOTRR-----PEVTPPHLS 198  
Db 842 TERLKSVEIRLTKVLKPADGRSLINPEAMPHTS 876

RESULT 7  
B48516  
surfactant protein A receptor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 07-Apr-1994  
C:Accession: B48516  
R;Strayer, D.S.; Yang, S.; Jerng, H.H.  
J. Biol. Chem. 268, 18679-18684, 1993  
A;Title: Surfactant protein A-binding proteins. Characterization and structures.  
A;Reference number: A48516; MUID:93366778; PMID:8360162  
A;Accession: B48516  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A;Residues: 1-284 <STR>  
A;Cross-references: GB:L10124

Query Match 8.4%; Score 88; DB 2; Length 284;  
Best Local Similarity 24.1%; Pred. No. 2.5;  
Matches 40; Conservative 24; Mismatches 62; Indels 40; Gaps 7;  
QY 27 LCAKAFESLFRDYDKDTTFQYFKSKRVIRNFNSNPLSAADARLRLHKTFLGKEMKLYFA 86  
Db 3 MCYGMGSLFRSGSRQTLFA-----SQVMRYAD-----LYAAGFIN---LLYYP 43

QY 87 QTLHGSSHLAPPN-----DKOFLISPPAS-----PPVGWKQVEDATPVINYDLLYAI 135  
Db 44 FSVLFRAAHVLMPIHSTVEHTHVDINEMESPLATRNRTSVDPKD-----TDYKRHQLTRSI 99  
QY 136 SKLGPEKYEHLAADTPTSPVVHVHVCSDQNEEEEMERMKRPK 181  
Db 100 SEIKPPNLFPL-----APQETHCHDEDDDEEEEBECCGKPK 139  
RESULT 8  
S29796  
hypothetical protein 2280 - evening primrose chloroplast (fragment)  
C:Species: chloroplast Oenothera villaricae (evening primrose)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: S29796; S19986  
R;Nimzyk, R.; Schoendorf, T.; Hachtel, W.  
Curr. Genet. 23, 265-270, 1993  
A;Title: In-frame length mutations associated with short tandem repeats are located in  
A;Reference number: S29795; MUID:93169690; PMID:8435856  
A;Accession: S29796  
A:Molecule type: DNA  
A;Residues: 1-630 <NIM>  
A;Cross-references: UNIPROT:P31569; EMBL:X64615; NID:gl4331; PID:gl4332  
C:Genetics:  
A;Genome: chloroplast  
C;Keywords: chloroplast

Query Match 8.4%; Score 88; DB 2; Length 630;  
Best Local Similarity 26.2%; Pred. No. 6.7;  
Matches 45; Conservative 23; Mismatches 48; Indels 56; Gaps 10;  
QY 16 CHLDP-RVFPV-DGLCRAKFESLFRDYDKDTTFQYFKSKRVIRNFNSNPLSAADARLRLHK 73  
Db 81 CSIDPISIVIKKNCAGDSSLVKWY-----FELGTSMKKLT----- 118  
QY 74 TFLGKEMKLYFAQTLLHIGS-----SHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130  
Db 119 -----LLYLLTCSAGSIAQDLLSPGPDQNLIT-----SYGLVEN-----DSD 157  
QY 131 LLVATSLGPGKEKYEHLAA---TDTPSPVVHVHVCSDQNEEEE---EEEME 175  
Db 158 LVHGLSDIVHG--LLEGLALVGSSPTTEEEVEGTEEEVEGTEEEVE 208

RESULT 9  
S29795  
hypothetical protein 2280 - evening primrose (Oenothera picensis subsp. picensis) chlor  
C:Species: chloroplast Oenothera picensis subsp. picensis (evening primrose)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: S29795; S19983  
R;Nimzyk, R.; Schoendorf, T.; Hachtel, W.  
Curr. Genet. 23, 265-270, 1993  
A;Title: In-frame length mutations associated with short tandem repeats are located in  
A;Reference number: S29795; MUID:93169690; PMID:8435856  
A;Accession: S29795  
A:Molecule type: DNA  
A;Residues: 1-721 <NIM>  
A;Cross-references: UNIPROT:P31568; EMBL:X64616; NID:gl4334; PID:gl4335  
C:Genetics:  
A;Genome: chloroplast  
C;Keywords: chloroplast

Query Match 8.4%; Score 88; DB 2; Length 721;  
Best Local Similarity 26.2%; Pred. No. 7.9;  
Matches 45; Conservative 23; Mismatches 48; Indels 56; Gaps 10;  
QY 16 CHLDP-RVFPV-DGLCRAKFESLFRDYDKDTTFQYFKSKRVIRNFNSNPLSAADARLRLHK 73  
Db 81 CSIDPISIVIKKNCAGDSSLVKWY-----FELGTSMKKLT----- 118  
QY 74 TFLGKEMKLYFAQTLLHIGS-----SHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130  
Db 119 -----LLYLLTCSAGSIAQDLLSPGPDQNLIT-----SYGLVEN-----DSD 157



QY 45 FOYFKSKVRINFSNPLSAADARLRHLKTEFLGKEMKLYFAOTLHIGSSHLAPPNP--- 101  
DB 450 FA .....SOMRYAD---LYAASFN---LLYPPSYLFRAAHVLMPHSTV 490  
QY 102 -----DKQFLISPPAS---PPVGKQVEDATPVINYDLVAISKLPGEKVELHAATDPT 153  
DB 491 EHTHVDINEMESPLATNRRTSVDFKD---TDYKRHLQTRTSISEIKPPNLFPL-----A 540  
QY 154 PSVVVHVCHESDQENEEEEEEME 175  
DB 541 PQEITH-CHDEDDDEEEEEE 561

RESULT 14  
T31421  
C-terminal domain-binding protein ral - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31421  
R:Yuryev, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord  
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996  
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts with  
A:Reference number: Z21024; MUID:96293459; PMID:8692929  
A:Accession: T31421  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1173 <YUR>  
A:Cross-references: UNIPROT:Q63624; EMBL:U49056; NID:gl438531; PID:gl438532; PIDN:AAC526  
A:Experimental source: hippocampus

Query Match 7.9%; Score 83; DB 2; Length 1173;  
Best Local Similarity 24.1%; Pred. No. 40;  
Matches 49; Conservative 18; Mismatches 88; Indels 48; Gaps 7;  
QY 1 MEEVDLQDLPSATIACHLD--PRFVVDGLCRKPFESLFTYDKDTTFQYFKSKVRINRF 58  
DB 14 VEVVSILDPDPTWVPSHLDPQSESDVL--ELVAEVRIGDRDP-----M 56  
QY 59 SNPLSAADARLRHLKTEFLGKEMK-----LYFAOTLHIGSSHLAPP-----N 100  
DB 57 PLEVPSSLPLRLAWRT--GKTVSPQSHASRRPACSRHLLTLGTGCGGAPPAPPSGSSS 113  
QY 101 PDKQFLISPPASPPVGKQVEDATPVINYDLVAISKI-----GPGEKVELHAATDP 152  
DB 114 PSFSPSSSPSPPP 173  
QY 153 TPSVVVHVCHESDQENEEEEEEME 175  
DB 174 NPSSSGGTGTPSEEEEEEEEEEE 196

RESULT 15  
E96752  
hypotheical protein F28P22.5 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E96752  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: E96752  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-697 <STO>

A:Cross-references: UNIPROT:Q9CAI9; GB:AE005173; NID:g6648152; PIDN:AAF21152.1; GSPDB:G  
C:Genetics:  
A:Gene: F28P22.5  
A:Map position: 1

Query Match 7.8%; Score 82; DB 2; Length 697;  
Best Local Similarity 24.7%; Pred. No. 26;  
Matches 44; Conservative 23; Mismatches 65; Indels 46; Gaps 7;

QY 40 DKDTTFQYFKS-----FKRVRIINPSNPLS-----AADARLRHLKTEFLGKEMK 82  
DB 291 DKDTTNQKENSQETPMSDEKIELPRALSRETOKTQSAAFQAAEIAKRIAKME--SQKRR 348  
QY 83 LYFAOTLHIGSSHLAPPNPKQFLISPPASPPVGKQVEDATPVINYDLVAIS---KLK 139  
DB 349 LLEMQA-----NLDKQMMFTTVSYRYSIKQVEDAT-----YGFSDALKIG 389  
QY 140 PGKVELHAATDPTSPVVHVCHESD-----QENEEEEEEMERMKRPKPKIOTRRPEY 192  
DB 390 EGGYGPVYKAVLDYTSVAIKILKSGITGLKQFQQBIEVLSSMRHPNMVILLGACPEY 447

Search completed: November 16, 2005, 17:13:06  
Job time : 14.15 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 16:32:05 ; Search time 49.5 Seconds  
(without alignments)  
2048.317 Million cell updates/sec

Title: US-09-575-580B-4

Perfect score: 1048

Sequence: 1 MBEVDLQDLPATSIAIHLDP.....RPKPKIIQRRPEYTPIHLS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_treml.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	99.2	198	1 CCPI_MOUSE	Q9jhg6 mus musculus
2	1040	99.2	251	2 Q7TNY3	Q7tny3 mus musculus
3	1002.5	95.7	197	1 CCPI_HUMAN	P53805 homo sapien
4	1002.5	95.7	252	2 Q7Z555	Q7z555 homo sapien
5	887.5	84.7	199	2 Q8K4S2	Q8k4s2 rattus norv
6	884.5	84.4	197	1 CCPI_CRIGR	O35847 cricetus
7	883.5	84.3	197	2 Q6XXM7	Q6xxm7 ovis aries
8	883.5	84.3	199	2 Q6IN33	Q6in33 rattus norv
9	847.5	80.9	242	2 Q6ZMM3	Q6zmm3 homo sapien
10	834.5	79.6	231	2 Q7ZXP4	Q7zxp4 xenopus lae
11	784.5	74.9	199	2 Q6DK90	Q6dk90 xenopus lae
12	777.5	74.2	199	2 Q7T0U1	Q7t0u1 xenopus lae
13	643.5	61.4	196	2 Q6DGB1	Q6dgb1 brachydanio
14	639.5	61.0	210	2 Q6DC33	Q6dc33 brachydanio
15	627.5	59.9	243	2 Q8VIP4	Q8vip4 mus musculus
16	622.5	59.4	243	2 Q8CH26	Q8ch26 rattus norv
17	618.5	59.0	230	2 Q6DG39	Q6dg39 brachydanio
18	613.5	58.5	197	1 CCP2_MOUSE	Q9jhg2 mus musculus
19	609.5	58.2	225	2 Q86YJ0	Q86yj0 homo sapien
20	608.5	58.1	192	2 Q8VIP5	Q8vip5 mus musculus
21	608.5	58.1	197	2 Q8CH27	Q8ch27 rattus norv
22	607.5	58.0	243	2 Q8N116	Q8n116 homo sapien
23	606.5	57.9	195	2 Q6NSN4	Q6nsn4 brachydanio
24	597	57.0	239	1 CCP3_MOUSE	Q9jkk0 mus musculus
25	596.5	56.9	197	1 CCP2_HUMAN	Q14206 homo sapien
26	596	56.9	241	1 CCP3_HUMAN	Q9uka8 homo sapien
27	379.5	36.2	292	1 SRA_DROME	Q9xz18 drosophila
28	351	33.5	207	1 CCPI_CAEAL	P53806 caenorhabdi
29	155	14.8	29	2 Q9HZAI	Q9hza1 homo sapien
30	139.5	13.3	315	2 Q9P5S9	Q9p5s9 neurospora
31	115.5	11.0	249	2 Q66PG0	Q66pg0 cryptococcus

32	114.5	10.9	249	2	Q9P4A1	Q9p4a1 cryptococcus
33	114.5	10.9	405	2	Q86JH9	Q86jh9 dictyosteli
34	106.5	10.2	264	2	Q6G6F1	Q6g6f1 yarrowia li
35	102	9.7	775	2	Q7SAZ0	Q7saz0 neurospora
36	95.5	9.1	163	1	YA9F_SCHPO	Q09791 schizosacch
37	94	9.0	318	2	Q8LFB4	Q8lfb4 arabidopsis
38	94	9.0	318	2	Q8VZ43	Q8vz43 arabidopsis
39	94	9.0	318	2	Q8SL96	Q8sl96 arabidopsis
40	93	8.9	227	2	Q6YX04	Q6yx04 oryza sativ
41	93	8.9	513	2	Q8ALP8	Q8alp8 bacteroides
42	92	8.8	328	2	Q9LSD3	Q9lsd3 arabidopsis
43	92	8.8	513	2	Q64ZB5	Q64zb5 bacteroides
44	92	8.8	992	2	Q9NTH6	Q9nth6 homo sapien
45	92	8.8	1456	2	Q9UPV0	Q9upv0 homo sapien

#### ALIGNMENTS

##### RESULT 1

CCPI\_MOUSE STANDARD: PRT; 198 AA.  
ID CCPI\_MOUSE Q9JHG6; Q9JWQ4; Q9JK50; Q9JK51; Q9JKK2; Q9JKK3;  
AC Q9JHG6; Q9JWQ4; Q9JK50; Q9JK51; Q9JKK2; Q9JKK3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Calcipressin 1 (Down syndrome critical region protein 1 homolog)  
DE (Myocyte-enriched calcineurin interacting protein 1) (MCIP1).  
DE Names=Dscr1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RC STRAIN=BALB/C; TISSUE=Brain;  
RX MEDLINE=20534792; PubMed=11080588; DOI=10.1016/S0378-1119(00)00407-8;  
RA Strippoli P., Petrini M., Lenzi L., Carinci P., Zannotti M.;  
RT "The murine DSCR1-like (Down syndrome candidate region 1) gene family:  
RT conserved synteny with the human orthologous genes.";  
RL Gene 257:223-232(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
RX MEDLINE=20187590; PubMed=10722714; DOI=10.1074/jbc.275.12.8719;  
RA Rothmel B., Vega R.B., Yang J., Wu H., Baesel-Duby R.,  
RA Williams R.S.;  
RT "A protein encoded within the Down syndrome critical region is  
RT enriched in striated muscles and inhibits calcineurin signaling.";  
RL J. Biol. Chem. 275:8719-8725(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM A), AND FUNCTION.  
RC TISSUE=Fetal brain;  
RX MEDLINE=21152220; PubMed=11231093; DOI=10.1016/S0925-4773(00)00583-9;  
RA Casas C., Martinez S., Pritchard M.A., Fuentes J.J., Nadal M.,  
RA Guinera J., Arbones M., Florez J., Soriano E., Estivill X.,  
RA Alcantara S.;  
RT "Dscr1, a novel endogenous inhibitor of calcineurin signaling, is  
RT expressed in the primitive ventricle of the heart and during  
RT neurogenesis.";  
RL Mech. Dev. 101:289-292(2001).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).  
RX Fuentes J.J., Pritchard M.A., Pucharcos C., Estivill X.;  
RT "Down syndrome candidate region 1 (Dscr1), one of three alternatively  
RT spliced exon 1 transcripts.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM C).  
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedziercki R.M., King B.L.,  
RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
RA Petrovskiy N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada M.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC TISSUE=Kidney;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner P.S., Schenker C.W., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses  
CC by binding to the catalytic domain of calcineurin A. Could play a  
CC role during central nervous system development.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist;  
CC Name=A; Synonyms=1;  
CC IsoId=Q9JHG6-1; Sequence=Displayed;  
CC Name=B; Synonyms=4;  
CC IsoId=Q9JHG6-2; Sequence=VSP\_001317;  
CC Name=C;  
CC IsoId=Q9JHG6-3; Sequence=VSP\_001318;  
CC -!- TISSUE SPECIFICITY: Highly expressed in heart and skeletal muscle.  
CC Also expressed in all other tissues.  
CC -!- SIMILARITY: Belongs to the DSCR1 family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; AF282255; AAF91461.1; -  
DR EMBL; AF237789; AAF63485.1; -  
DR EMBL; AF237790; AAF63486.1; -  
DR EMBL; AF260717; AAF70343.1; -  
DR EMBL; AF263233; AAF72701.1; -  
DR EMBL; AF263240; AAF72702.1; -  
DR EMBL; AK010696; BAB27128.1; -  
DR EMBL; BC013551; AAH13551.1; -  
DR MGD; MGI:1890564; Dscr1.  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR InterPro; IPR006931; Calcipressin.  
DR Pfam; PF04847; Calcipressin; 1.  
KW Alternative splicing.  
FT VARSPLIC 1 28  
FT MEEVDQLPSATIAIACHLDPRVFDGLC -> MHFRDPSYN  
FT FSSLIACVANDDVSESET (in isoform B).  
FT /FTId=VSP\_001317.  
FT Missing (in isoform C).  
FT /FTId=VSP\_001318.  
FT T -> P (in Ref. 2).  
FT CONFLICT 152 152  
FT SEQUENCE 198 AA; 22706 MW; BA35340AFD6F0582 CRC64;  
SQ  
Query Match 99.2%; Score 1040; DB 1; Length 198;  
Best Local Similarity 99.5%; Pred. No. 8.7e-81;  
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MEEVDQLPSATIAIACHLDPRVFDGLCRAPESLFRYVDKDTTFQYFKSKVRINFN 60  
DB 1 MEEVDQLPSATIAIACHLDPRVFDGLCRAPESLFRYVDKDTTFQYFKSKVRINFN 60  
QY 61 PLISAADARLRHKTFLGKEMKLYPAQTLHGSSHLAPNDPKQFLISPPASPPVGVKQV 120  
DB 61 PLISAADARLRHKTFLGKEMKLYPAQTLHGSSHLAPNDPKQFLISPPASPPVGVKQV 120  
QY 121 EDATPVINDLLYALSKLPGCKEYELHAATPTPSVVHVVCSDQENEEEMERMKRP 180  
DB 121 EDATPVINDLLYALSKLPGCKEYELHAATPTPSVVHVVCSDQENEEEMERMKRP 180  
QY 181 KPFIQTRRPEYTPHLS 198  
DB 181 KPFIQTRRPEYTPHLS 198  
RESULT 2  
Q7TNY3  
ID Q7TNY3 PRELIMINARY; PRT; 251 AA.  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Calcipressin 1 large isoform.  
GN Name=Dscr1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NIH/Swiss; TISSUE=Heart;  
RX MEDLINE=2806131; PubMed=12809556; DOI=10.1042/BJ20030267;  
RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,  
RA Perez-Riba M.;  
RT "Phosphorylation of calcipressin 1 increases its ability to inhibit  
RT calcineurin and decreases calcipressin half-life.";  
RL Biochem. J. 374:567-575 (2003).  
DR EMBL; AY325904; AAP96744.1; -  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR InterPro; IPR006931; Calcipressin.  
DR Pfam; PF04847; Calcipressin; 1.  
DR SEQUENCE 251 AA; 28137 MW; 09F47C73D847FB2B CRC64;  
SQ

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Query Match          99.2%; Score 1040; DB 2; Length 251;
Best Local Similarity 99.5%; Pred. No. 1.2e-80;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEEVDLQDLPSATIACHLDRPVVDGLCRAKFSLFRTYDKDTTFQYFKSFKRVRINFNS 60
DB 54 MEEVDLQDLPSATIACHLDRPVVDGLCRAKFSLFRTYDKDTTFQYFKSFKRVRINFNS 113

QY 61 PLSAADARLRHLKTEFLGKEMKLYFAQTLHGSHLAPPNDPKQFLISPPASPPVGVKQV 120
DB 114 PLSAADARLRHLKTEFLGKEMKLYFAQTLHGSHLAPPNDPKQFLISPPASPPVGVKQV 173

QY 121 EDATPVINDLLYAIKSLGPGKGYELHAATDTPPSVVHVHVCSDQNEEEEMERMKRP 180
DB 174 EDATPVINDLLYAIKSLGPGKGYELHAATDTPPSVVHVHVCSDQNEEEEMERMKRP 233

QY 181 KPKIOTRRPEYTPIHLS 198
DB 234 KPKIOTRRPEYTPIHLS 251

RESULT 3
CCPI_HUMAN
ID CCPI_HUMAN STANDARD; PRT; 197 AA.
AC P53805; O00582; O00583; Q96R03; Q9BU69; Q9UF15; Q9UME4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 1 (Down syndrome critical region protein 1) (Myocyte-
enriched calcineurin interacting protein 1) (MCIP1) (Adapt78).
GN Name=DSCR1; Synonyms=ADAPT78, DSC1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RX MEDLINE=96121593; PubMed=8595418;
RA Fuentes J.-J., Pritchard M.A., Planas A.M., Bosch A., Ferrer I.,
RA Estivill X.;
RT "A new human gene from the Down syndrome critical region encodes a
RT proline-rich protein highly expressed in fetal brain and heart.";
RL Hum. Mol. Genet. 4:1935-1944(1995).
RN [2]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=97468152; PubMed=9325060; DOI=10.1006/geno.1997.4866;
RA Fuentes J.-J., Pritchard M.A., Estivill X.;
RT "Genomic organization, alternative splicing, and expression patterns
of the DSCR1 (Down syndrome candidate region 1) gene.";
RL Genomics 44:358-361(1997).
RN [3]
SEQUENCE FROM N.A. (ISOFORM 3).
RA Hua F., Wu J., Zhou Y., Zhang B., Peng X., Qiang B., Yuan J.,
RA Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=bung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
SEQUENCE OF 1-164 FROM N.A. (ISOFORM 2).
RP TISSUE=Breast;
RC Crawford D.R., Leahy K.P., Davies K.J.A.;
RA "Adapt78, a calcium and oxidant-inducible RNA.";
RT Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
CHARACTERIZATION.
RX MEDLINE=20320698; PubMed=10861295; DOI=10.1093/hmg/9.11.1681;
RA Fuentes J.-J., Genesca L., Kingsbury T.J., Cunningham K.W.,
RA Perez-Riba M., Estivill X., de la Luna S.;
RT "DSCR1, overexpressed in Down syndrome, is an inhibitor of
calcineurin-mediated signaling pathways.";
RL Hum. Mol. Genet. 9:1681-1690(2000).
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
by binding to the catalytic domain of calcineurin A. Could play a
role during central nervous system development.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=P53805-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P53805-2; Sequence=VSP_001314;
CC Name=3;
CC IsoId=P53805-3; Sequence=VSP_001315;
CC Name=4;
CC IsoId=P53805-4; Sequence=VSP_001316;
CC -!- TISSUE SPECIFICITY: Highly expressed heart, brain and skeletal
muscle. Also expressed in all other tissues.
CC -!- INDUCTION: By calcium.
CC -!- SIMILARITY: Belongs to the DSCR1 family.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; U28833; AAB81557.1; -
CC EMBL; U85265; AAB84370.1; -
CC EMBL; U85266; AAB84371.2; -
CC EMBL; U85267; AAB84372.1; -
CC EMBL; AF400423; AAB92478.1; -
CC EMBL; BC002864; AAB02864.1; -
CC EMBL; U53821; AAF21218.1; -
CC Genew; HGNC:3040; DSCR1.
CC H-InvDB; HIX0016091; -
CC MIM; 602917; -
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0003700; P:transcription factor activity; TAS.
CC GO; GO:0007417; P:central nervous system development; TAS.
CC GO; GO:0008015; P:circulation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR006931; Calcipressin.
CC Pfam; PF04847; Calcipressin; 1.
CC Alternative splicing.
CC DOMAIN 156 174
CC VARSPLIC 1 28
CC
CC VARSPLIC 1 29
CC
CC VARSPLIC 1 80
CC
CC Missing (in isoform 4).
CC /FTID=VSP_001315.
CC /FTID=VSP_001316.
```

FT CONFLICT 147 147 H -> R (in Ref. 3).  
 FT CONFLICT 159 159 H -> Q (in Ref. 5).  
 SQ SEQUENCE 197 AA; 22637 MW; 1BD426BB88167B6C CRC64;

Query Match 95.7%; Score 1002.5; DB 1; Length 197;  
 Best Local Similarity 96.5%; Pred. No. 1.4e-77;  
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MEEVDLQDLPSATIACHLDPVFDGLCRKAKFESLFRITYDKDITTFQYFKSFRRVINFNSN 60  
 DB 1 MEEVDLQDLPSATIACHLDPVFDGLCRKAKFESLFRITYDKDITTFQYFKSFRRVINFNSN 60  
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHIGSSHLAPPNDPKQLISPPASPPVGVKQV 120  
 DB 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHIGSSHLAPPNDPKQLISPPASPPVGVKQV 120  
 QY 121 EDATPVINDLYAIKSGPGKGYELHAATDTPSVVHVHVCSDQENEEEMERMKRP 180  
 DB 121 EDATPVINDLYAIKSGPGKGYELHAATDTPSVVHVHVCSDQENEEEMERMKRP 179  
 QY 181 KPKIOTRRPEYTPIHLS 198  
 DB 180 KPKIOTRRPEYTPIHLS 197

RESULT 4  
 QY2555 ID Q72555 PRELIMINARY; PRT; 252 AA.  
 AC Q72555;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Calcipressin 1 large isoform.  
 GN Name=DSCR1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=22806131; PubMed=12809556; DOI=10.1042/BJ20030267;  
 RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,  
 RA Perez-Riba M.;  
 RT "Phosphorylation of calcipressin 1 increases its ability to inhibit  
 RT calcineurin and decreases calcipressin half-life.";  
 RL Biochem. J. 374:567-575(2003).  
 DR EMBL; AV325903; AAP96743.1; -;  
 DR GO; GO:0019722; P:calcium-mediated signaling; IEA.  
 DR InterPro; IPR006931; Calcipressin.  
 DR Pfam; PF04847; Calcipressin; 1.  
 SQ SEQUENCE 252 AA; 28078 MW; 0B17133D03BD7AFA CRC64;

Query Match 95.7%; Score 1002.5; DB 2; Length 252;  
 Best Local Similarity 96.5%; Pred. No. 1.9e-77;  
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MEEVDLQDLPSATIACHLDPVFDGLCRKAKFESLFRITYDKDITTFQYFKSFRRVINFNSN 60  
 DB 56 MEEVDLQDLPSATIACHLDPVFDGLCRKAKFESLFRITYDKDITTFQYFKSFRRVINFNSN 115  
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHIGSSHLAPPNDPKQLISPPASPPVGVKQV 120  
 DB 116 PLSAADARLRLHKTFLGKEMKLYFAQTLHIGSSHLAPPNDPKQLISPPASPPVGVKQV 175  
 QY 121 EDATPVINDLYAIKSGPGKGYELHAATDTPSVVHVHVCSDQENEEEMERMKRP 180  
 DB 176 EDATPVINDLYAIKSGPGKGYELHAATDTPSVVHVHVCSDQENEEEMERMKRP 234  
 QY 181 KPKIOTRRPEYTPIHLS 198  
 DB 235 KPKIOTRRPEYTPIHLS 252

RESULT 5  
 QYK4S2 ID Q8K4S2 PRELIMINARY; PRT; 199 AA.  
 AC Q8K4S2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myocyte-enriched calcineurin-interacting protein 1.  
 GN Name=mcip 1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Odashima M., Nagata K., Obata K., Somura F., Izawa H., Miyazaki T.,  
 RA Murata Y., Seo H., Yamada Y., Yokota M.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB075973; BAC06443.1; -;  
 DR GO; GO:0019722; P:calcium-mediated signaling; IEA.  
 DR InterPro; IPR006931; Calcipressin.  
 DR Pfam; PF04847; Calcipressin; 1.  
 SQ SEQUENCE 199 AA; 22976 MW; 94A311E6GD59F0B9 CRC64;

Query Match 84.7%; Score 887.5; DB 2; Length 199;  
 Best Local Similarity 91.5%; Pred. No. 9e-68;  
 Matches 173; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 11 SATIACHLDPVFDGLCRKAKFESLFRITYDKDITTFQYFKSFRRVINFNSPLSAADARLR 70  
 DB 11 SSLIACVANGDVFSSETRAKFESLFRITYDKDITTFQYFKSFRRVINFNSPLSAADARLR 70  
 QY 71 LHKTEFLGKEMKLYPAOTLHIGSSHLAPPNDPKQLISPPASPPVGVKQVEDATPVIND 130  
 DB 71 LHKTEFLGKEMKLYPAOTLHIGSSHLAPPNDPKQLISPPASPPVGVKQVEDATPVIND 130  
 QY 131 LLYAISKLGPGEKGYELHAATDTPSVVHVHVCSDQ-ENEEEMERMKRPKPKIIQTRR 189  
 DB 131 LLYAISKLGPGEKGYELHAATDTPSVVHVHVCSDQEEEEEEMERMKRPKPKIIQTRR 190  
 QY 190 PEYTPIHLS 198  
 DB 191 PEYTPIHLS 199

RESULT 6  
 CCPI\_CRIGR ID CCPI\_CRIGR STANDARD; PRT; 197 AA.  
 AC O35847;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Calcipressin 1 (Down syndrome critical region protein 1 homolog)  
 DE (Oxidative-induced protein Adapt78).  
 GN Name=DSCR1; Synonyms=ADAPT78;  
 OS Cricetulus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus  
 OX NCBI\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97329095; PubMed=9185608; DOI=10.1006/abbi.1997.0109;  
 RA Crawford D.R., Leahy K.P., Abramova N., Lan L., Wang Y., Davies K.J.;  
 RA "Hamster adapt78 mRNA is a Down syndrome critical region homologue  
 RT that is inducible by oxidative stress.";  
 RL Arch. Biochem. Biophys. 342:6-12(1997).  
 CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses  
 CC by binding to the catalytic domain of calcineurin A. Could play a  
 CC role during central nervous system development (By similarity).  
 CC -!- INDUCTION: By oxidative stress.  
 CC -!- SIMILARITY: Belongs to the DSCR1 family.



Db 131. LLVAISKLGPGKYEHLHAATDTTSPVVHVCSQDEN-EEDEMERMKRPKPIQTRRP 189

Qy 191 EYTPIHLS 198  
|||||

Db 190 EYTPIHLS 197

ID	Q6IN33	PRELIMINARY;	PRT;	199 AA.
AC	Q6IN33;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	Down syndrome critical region homolog 1.			

03-JUN-2004 (Armbrester, 27, Last annotation update)  
 DE Down syndrome critical region homolog 1.  
 DI  
 DN  
 OS Rattus norvegicus (Rat).  
 OS Name=Dscr1;  
 GN  
 OS  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC  
 NCBI\_TaxId=10116;  
 [1]  
 RN  
 RP SEQUENCE FROM N.A.

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
	[1]
RN	SEQUENCE FROM N.A.
RP	
RC	TISSUE=Heart;

RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M., Uding T.B., Tomlinson S., Carninci P., Deane C.

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeslee P.W., Touchman J.W., Green E.D., Dickson M.C.

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;

RA Arzywinski M.A., Skabala U., Smaluk D.B., Scimerin A., Schemm J.S.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
SEQUENCE FROM N.A.  
RC  
TISSUE=Heart;  
Straussberg R.;  
submitted (JUN-2004) to the EMBL/GenBank/DBPJ databases

RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC072478; AAH72478.1; -.  
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.  
DR InterPro; IPR006931; Calcipressin.

DR GO; GO:0013722; P:calcium-mediated signaling; IEA.  
DR InterPro; IPR006931; Calcipressin.  
DR Pfam; PF04847; Calcipressin; 1.  
SQ SEQUENCE 199 AA; 22948 MW; 3BA20EE4BD59F0BB CRC64;  
Query Match 84 33. Score 883 5. DB 2. Length 199.

Query Match 84.3%; Score 883.5; DB 2; Length 199;  
Best Local Similarity 91.0%; Pred. No. 2e-67;  
Matches 172; Conservative 4; Mismatches 12; Indels 1; Gaps 1

[illegible]

Db	11	SSLIACVANGDVFESESETRAFESLPTDYKDITFYQFKSFKVRINFSNPLSAADARLQ	70
Qy	71	LHKTEFLGKMKLYFAQTLHGSSHLAPPNDKQLISPSPVPGWKQVEDATPTVINYD	130
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Db	71	LHKTBFGLGKMKLYFAQT	LHGSSHLAPPNDKQFLISPPAPVGVKQVEDATPVINYD	130
Qy	131	LLYAIKLGPEKVELHAAT	PTSPVVHVHVESDQ-ENESESESEMERKRPKPKIIQTRR	189
Db	131	LLYAIKLGPEKVELHAAT	TTTPSVVVHVHVESDQSESESESESEMERKRPKPKIIQTRR	190

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Db      131  L Y A T S K G P G E K Y E L H A A T D T T S V V H V C S D Q E E E E E E M E R M K R P K P I I Q T R R 190
Qy      190  P E Y T P I H L S 198
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Db      191 PEYTPHLS 199
RESULT 9
Q62MW3 PRELIMINARY; PRT; 242 AA.
AC Q62MW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16823.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Negahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131569; BAD18702.1; -.
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
SQ SEQUENCE 242 AA; 27850 MW; 4888F4EAB303BA81 CRC64;

Query Match 80.9%; Score 847.5; DB 2; Length 242;
Best Local Similarity 83.2%; Pred. NO. 3e-64;
Matches 164; Conservative 12; Mismatches 14; Indels 7; Gaps 2;

QY 8 DLPSATIACHLDPRVFDGLC-----RAKFSLERTYDKDTTFQYFKSKVRINFSP 61
Db NIPEDTLLSYPESSLPQRHCAFHRSKAKFSLERTYDKDTTFQYFKSKVRINFSP 106
QY 62 LSAADARLRHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGWKQVE 121
Db FSAADARLRHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGWKQVE 166
QY 122 DATPVINYDLLVAISKLGPGEKLYELHAATDTPSVVVHVCSDOENE-EBEEMERMKRP 181
Db DATPVINYDLLVAITKLGPGKLYELHAATDTPSVVVHVCSDOE-KEBEEMERMRPK 225
QY 182 PKLIOTRRPEYTPHLS 198
Db PKLIOTRRPEYTPHLS 242

RESULT 10
Q7ZXP4 PRELIMINARY; PRT; 231 AA.
AC Q7ZXP4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Decrl-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:56 ; Search time 125.95 Seconds  
(without alignments)  
743.120 Million cell updates/sec

Title: US-09-575-580B-5

Perfect score: 1296

Sequence: 1 EFVDPVRPRVRLGQOASIP.....TSPKPKINQTRRGLPPFGH 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Genesecp1980s:\*
- 2: Genesecp1990s:\*
- 3: Genesecp2000s:\*
- 4: Genesecp2001s:\*
- 5: Genesecp2002s:\*
- 6: Genesecp2003as:\*
- 7: Genesecp2003bs:\*
- 8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1129	87.1	234	4 AAB31788	Aab31788 Amino aci
2	1129	87.1	243	7 ADB64062	Adb64062 Human pro
3	1129	87.1	255	5 AAM50760	Aam50760 Human Dow
4	1129	87.1	255	7 ADE37339	Ade37339 Human Dow
5	882	68.1	197	5 AAE18913	Aae18913 Mouse MCI
6	861	66.4	197	6 ABO07172	Abo07172 Human p53
7	848	65.4	192	5 AAE18916	Aae18916 Human MCI
8	848	65.4	192	7 ADE37341	Ade37341 Human Dow
9	708.5	54.7	241	5 AAE18917	Aae18917 Human MCI
10	708.5	54.7	241	6 ABO07173	Abo07173 Human p53
11	708.5	54.7	241	7 ADE37342	Ade37342 Human Dow
12	676.5	52.2	252	5 AAE18918	Aae18918 Human MCI
13	648	50.0	252	7 ADB64738	Adb64738 Human pro
14	616	47.5	197	5 AAE18915	Aae18915 Human MCI
15	616	47.5	197	5 AAE18914	Aae18914 Human MCI
16	616	47.5	197	7 ADE25770	Ade25770 Human pro
17	616	47.5	197	8 ADRI4119	Adri4119 Human NF-
18	613.5	47.3	198	5 AAE18912	Aae18912 Mouse MCI
19	606.5	46.8	198	5 AAE18911	Aae18911 Human MCI
20	582	44.9	242	8 ADRI0481	Adri0481 Human pro
21	565	43.6	171	2 AAW73898	Aaw73898 Human Dow
22	418.5	32.3	292	4 ABB71467	Abb71467 Drosophila
23	312	24.1	111	3 AAG01768	Aag01768 Human sec
24	289	22.3	142	3 AAB58452	Aab58452 Lung canc
25	213	16.4	58	4 AAM15671	Aam15671 Peptide #

ALIGNMENTS

RESULT 1

AAB31788

ID AAB31788 standard; protein; 234 AA.

XX AAB31788;

XX AC

XX 30-APR-2001 (first entry)

XX

DE Amino acid sequence of a human detoxification protein.

XX Human; detoxification protein; DEXT; cancer; leukaemia; melanoma;  
KW adenocarcinoma; autoimmune disorder; inflammatory disorder;  
KW rheumatoid arthritis; asthma; atherosclerosis; autoimmune thyroiditis;  
KW psoriasis; ulcerative colitis; infection; cell proliferative disorder;  
KW actinic keratosis; arteriosclerosis; cirrhosis; hepatitis.  
XX Homo sapiens.  
XX

Location/Qualifiers

Key Peptide 1..27  
FT /note= "signal peptide"  
FT Modified-site 58  
FT Modified-site 75 /note= "potential phosphorylation site"  
FT Modified-site 87 /note= "potential phosphorylation site"  
FT Modified-site 94 /note= "potential phosphorylation site"  
FT Modified-site 130 /note= "potential glycosylation site"  
FT Modified-site 204 /note= "potential phosphorylation site"  
FT Modified-site 215 /note= "potential phosphorylation site"  
FT Modified-site 223 /note= "potential phosphorylation site"  
FT /note= "potential phosphorylation site"

WO200104305-A2.

18-JAN-2001.

06-JUL-2000; 2000WO-US018509.

07-JUL-1999; 99US-0142678P.

(INCY-) INCYTE GENOMICS INC.

XX

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PI Tang YT, Yue H;
XX WPI; 2001-147193/15.
DR N-PSDB; AAF25338.
XX
XX New human detoxification protein and polynucleotide, useful for
PT diagnosis, prevention and treatment of autoimmune/inflammatory disorders
PT and cell proliferative disorders including cancer.
XX
XX Claim 1; Page 77; 79pp; English.
XX
XX The present sequence represents a human detoxification polypeptide
CC (DCTX). DCTX and its (ant)agonists are useful for preventing or treating
CC disorders associated with decreased or increased expression or activity
CC of DCTX. DCTX polypeptides are useful for screening compounds that
CC specifically binds to DCTX and for identifying (ant)agonists. Diseases
CC prevented, treated and diagnosed include cancers (e.g. leukaemia,
CC melanoma, adenocarcinoma, cancers of the brain, bone marrow, breast,
CC kidney, liver, pancreas, prostate and uterus), autoimmune/inflammatory
CC disorders (e.g. rheumatoid arthritis, asthma, atherosclerosis, autoimmune
CC thyroiditis, psoriasis and ulcerative colitis), bacterial, fungal,
CC parasitic infections and cell proliferative disorders (e.g. actinic
CC keratosis, arteriosclerosis, cirrhosis and hepatitis). Anti-DCTX
CC antibodies may be used as antagonists, as a targeting or delivery
CC mechanism for bringing pharmaceutical agents into contact with cells or
CC tissues expressing DCTX and for diagnosis of DCTX-related disorders
XX
XX Sequence 234 AA;
SQ
Query Match 87.1%; Score 1129; DB 4; Length 234;
Best Local Similarity 92.5%; Pred. No. 3.7e-111;
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 14 GQASIPEDGGFLFLCCIDRDWAVTQCPAEAFQALTFDPSLNFACNVHQSVEEEE 73
Db 5 GQGHVPEDGGFLFLCCIDRDWAVTQCPAEAFQALTFDPSLNFACNVHQSVEEEE 64
QY 74 SKEKEGLFRTYDECVTFQPKFSFRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 133
Db 65 SKEKEGLFRTYDDCVTFQPKFSFRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 124
QY 134 VQTPETDGDGKLHAPPQPAKQFLISPPSSPSVGMKPISDATPVLYNYDLLYAVAKLGPGEK 193
Db 125 VQTPETDGDGKLHAPPQPAKQFLISPPSSPPVGMQPINDDATPVLYNYDLLYAVAKLGPGEK 184
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINOTRRPGLPP 239
Db 185 YELHAGTESTPSVVHVCDSDIEREDPKTSPKPKIQTRRPGLP 230
RESULT 2
ID ADB64062
XX ADB64062 standard; protein; 243 AA.
AC ADB64062;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human protein encoded by clone BRAWH20014590.
XX
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
XX Homo sapiens.
XX
XX EP1308459-A2.
XX
XX 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
XX

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PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Maeuho Y;
XX
XX WPI; 2003-450961/43.
DR N-PSDB; ADB62092.
DR
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
XX Claim 1; Page; 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
XX Sequence 243 AA;
SQ
Query Match 87.1%; Score 1129; DB 7; Length 243;
Best Local Similarity 92.5%; Pred. No. 3.9e-111;
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 14 GQASIPEDGGFLFLCCIDRDWAVTQCPAEAFQALTFDPSLNFACNVHQSVEEEE 73
Db 14 GQGHVPEDGGFLFLCCIDRDWAVTQCPAEAFQALTFDPSLNFACNVHQSVEEEE 73
QY 74 SKEKEGLFRTYDECVTFQPKFSFRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 133
Db 74 SKEKEGLFRTYDDCVTFQPKFSFRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 133
QY 134 VQTPETDGDGKLHAPPQPAKQFLISPPSSPSVGMKPISDATPVLYNYDLLYAVAKLGPGEK 193
Db 134 VQTPETDGDGKLHAPPQPAKQFLISPPSSPPVGMQPINDDATPVLYNYDLLYAVAKLGPGEK 193
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINOTRRPGLPP 239
Db 194 YELHAGTESTPSVVHVCDSDIEREDPKTSPKPKIQTRRPGLP 239
RESULT 3
ID AAM50760
XX AAM50760 standard; protein; 255 AA.
AC AAM50760;
XX

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Db 86 SKEKPEGLFRTYDDCVTFQLFKSFRRVRINFSPKSAARARIELHETQFRGKKLKLKLYFAQ 145

QY 134 VQTPTDGDGKLHLAPPQAKQFLISPPSPVGVKWDISATPVNLYDLLYAVAKLGPGBK 193

Db 146 VQTPTDGDGKLHLAPPQAKQFLISPPSPVGVKWDISATPVNLYDLLYAVAKLGPGBK 205

QY 194 YELHAGTESTPSPVVHVCDSDMEREDPKTSKPKKINQTRRGLPP 239

Db 206 YELHAGTESTPSPVVHVCDSDIEEEDPKTSKPKKIQTRRGLPP 251

RESULT 5

AAE18913

ID AAE18913 standard; protein; 197 AA.

XX

AC AAE18913;

XX

DT 17-MAY-2002 (first entry)

XX

DE Mouse MCIP associated proein #4.

XX

KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;

KW heart failure; cardiomyopathy; heart disease; mouse.

XX

OS Mus musculus.

XX

PN WO200204491-A2.

XX

PD 17-JAN-2002.

XX

PF 06-JUL-2001; 2001WO-US021662.

XX

PR 07-JUL-2000; 2000US-0216601P.

XX

PR 13-FEB-2001; 2001US-00782953.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

PA (WILL/) WILLIAMS S R.

PA (ROTH/) ROTHERMEL B.

XX

PI Williams SR, Rothermel B;

XX

DR WPI: 2002-179698/23.

DR N-PSDB; AAD30154.

XX

PT Screening for modulators of muscle calcineurin interacting protein (MCIP)

PT binding, expression or phosphorylation, useful for treating cardiac

PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a

PT test compound.

PS Disclosure; Page 154; 174pp; English.

XX

CC The invention relates to muscle calcineurin interacting proteins (MCIPs)

CC and nucleic acid molecules encoding such proteins. MCIPs form a physical

CC complex with the catalytic subunit of calcineurin and increased levels of

CC MCIPs correspond to a reduced ability of calcineurin to stimulate

CC transcription of certain target genes. The invention also relates to

CC methods for identifying modulators of MCIP binding, expression or

CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin

CC may be used for treating cardiac hypertrophy and heart failure.

CC Antibodies to MCIP can be used in characterising the MCIP content of

CC healthy and diseased tissues and subsequently for determining the

CC presence or absence of cardiomyopathy or as predictor of heart disease.

CC The present sequence is mouse MCIP associated protein. Note: This

CC sequence has been described as mouse MCIP2 encoding DNA in the

CC specification, however the sequence seems to be a MCIP associated protein

XX

SQ Sequence 197 AA;

Query Match 68.1%; Score 882; DB 5; Length 197;

Best Local Similarity 91.8%; Pred. No. 5.2e-85;

Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 57 NSLFACNVHQSVFEEESKEKFEGLFRTYDECVTQFLFKSFRRVRINFSPKSAARARIE 116

Db 11 STLVAACVVDDVEFTNQEVKEKPEGLFRTYDECVTQFLFKSFRRVRINFSPKSAARARIE 70

QY 117 LHETQFRGKKLPLYFAQVQTPTDGDGKLHLAPPQAKQFLISPPSPVGVKWDISATPV 176

Db 71 LHETQFRGKKLPLYFAQVQTPTDGDGKLHLAPPQAKQFLISPPSPVGVKWDISATPV 130

QY 177 LNYDLLYAVAKLGPGEKYLHAGTESTPSPVVHVCDSDMEREDPKTSKPKKINQTRRP 236

Db 131 LNYDLLYAVAKLGPGEKYLHAGTESTPSPVVHVCDSDMEREDPKTSKPKKIQTRRP 190

QY 237 LPP 239

Db 191 LPP 193

RESULT 6

ABO07172

ID ABO07172 standard; protein; 197 AA.

XX

AC ABO07172;

XX

DT 13-AUG-2003 (first entry)

XX

DE Human p53 modifying protein, SEQ ID 132.

XX

KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;

KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;

KW lung cancer; ovarian cancer; angiogenesis; cell cycle;

KW apoptotic disorder; cell proliferation disorder.

XX

OS Homo sapiens.

XX

PN WO200299122-A1.

XX

PD 12-DEC-2002.

XX

PF 03-JUN-2002; 2002WO-US017382.

XX

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

XX

PA (EXEL-) EXELIXIS INC.

XX

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX

DR WPI: 2003-156859/15.

DR N-PSDB; ACD13348.

XX

PT Identifying modulators of the p53 pathway for use in treating apoptotic

PT or cell proliferation disorders, comprises screening for agents that

PT modulate activity of a human ortholog of genes that modify the p53

PT pathway in Drosophila.

XX

XX Example 2; Page 434-435; 678pp; English.

PS

CC The invention relates to identifying (M1) a candidate p53 pathway

CC modulating agent, by contacting an assay system comprising a purified HM

CC polypeptide (human orthologue of genes that modify the p53 pathway in

CC Drosophila) or nucleic acid with a test agent under conditions, where but

CC for the presence of the test agent, the system provides a reference

CC activity, and detecting a test agent-biased activity of a cell (comprising

CC Also included are modulating (M2) a p53 pathway of a cell (comprising

CC contacting a cell defective in p53 function with a candidate modulator

CC that specifically binds to a HM polypeptide comprising an HM amino acid

CC sequence, where p53 function is restored), modulating (M3) a p53 pathway

CC in a mammalian cell (comprising contacting the cell with an agent that

CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)

CC a disease in a patient (comprising: (a) obtaining a biological sample

CC from the patient; (b) contacting the sample with a probe for HM

CC expression; (c) comparing the results with a control; and (d) determining

CC whether the comparison indicates a likelihood disease). (M1) is useful

CC for identifying modulators of the p53 pathway. A probe for HM expression  
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,  
 CC in a patient, where the cancer has greater than 25 % expression level.  
 CC Modulators identified by (M1) are useful in a variety of diagnostic and  
 CC therapeutic applications, where disease or disorder prognosis is related  
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell  
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and  
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring  
 CC the p53 function of the cell, so that the cell undergoes normal  
 CC proliferation or progression through the cell cycle. (M2) and (M3) are  
 CC also useful for treating defects in the p53 pathway such as angiogenic,  
 CC apoptotic or cell proliferation disorders. The present sequence  
 CC represents a human p53 pathway modifying protein  
 XX  
 SQ Sequence 197 AA;

Query Match 66.4%; Score 861; DB 6; Length 197;  
 Best Local Similarity 89.1%; Pred. No. 8.9e-83;  
 Matches 163; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
 QY 57 NSLFACNVHQSVPFEESKEKEGFLRTYDECVTTFQLEKSFRRVRINFNSPKSAARARIE 116  
 DB 11 STLVACVDVVEFTNQEVKEKEGFLRTYDCCVTTFQLEKSFRRVRINFNSPKSAARARIE 70  
 QY 117 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGVKPISDATPV 176  
 DB 71 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGVKPISDATPV 130  
 QY 177 LNYDLLYAVAKLPGGKYLHAGTSTPSVHVHVCSDMEREDPKTSPKPKINQTRRPG 236  
 DB 131 LNYDLLYAVAKLPGGKYLHAGTSTPSVHVHVCSDMEREDPKTSPKPKINQTRRPG 190  
 QY 237 LPP 239  
 DB 191 LPP 193

RESULT 7  
 AAE18916  
 ID AAE18916 standard; protein; 192 AA.  
 XX  
 AC AAE18916;  
 XX  
 DT 17-MAY-2002 (first entry)  
 XX  
 DE Human MCIP associated protein #3.  
 XX  
 KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
 KW heart failure; cardiomyopathy; heart disease; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200204491-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001; 2001WO-US021662.  
 XX  
 PR 07-JUL-2000; 2000US-0216601P.  
 PR 13-FEB-2001; 2001US-00782953.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (WILL/) WILLIAMS S R.  
 PA (ROTH/) ROTHERMEL B.  
 XX  
 PI Williams SR, Rothermel B;  
 XX  
 DR WPI; 2002-179698/23.  
 DR N-PSDB; AAD30157.  
 XX  
 XX Screening for modulators of muscle calcineurin interacting protein (MCIP)  
 PT binding, expression or phosphorylation, useful for treating cardiac  
 PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a

PT test compound.  
 XX  
 PS Example 1; Page 165-166; 174pp; English.  
 XX  
 CC The invention relates to muscle calcineurin interacting proteins (MCIPs)  
 CC and nucleic acid molecules encoding such proteins. MCIPs form a physical  
 CC complex with the catalytic subunit of calcineurin and increased levels of  
 CC MCIPs correspond to a reduced ability of calcineurin to stimulate  
 CC transcription of certain target genes. The invention also relates to  
 CC methods for identifying modulators of MCIP binding, expression or  
 CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin  
 CC may be used for treating cardiac hypertrophy and heart failure.  
 CC Antibodies to MCIP can be used in characterising the MCIP content of  
 CC healthy and diseased tissues and subsequently for determining the  
 CC presence or absence of cardiomyopathy or as predictor of heart disease.  
 CC The present sequence is human MCIP associated protein. Note: This  
 CC sequence has been described as human MCIP splice variant in  
 CC specification, however the sequence seems to be a MCIP associated protein  
 XX  
 SQ Sequence 192 AA;

Query Match 65.4%; Score 848; DB 5; Length 192;  
 Best Local Similarity 88.0%; Pred. No. 2.1e-81;  
 Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;  
 QY 57 NSLFACNVHQSVPFEESKEKEGFLRTYDECVTTFQLEKSFRRVRINFNSPKSAARARIE 116  
 DB 6 STLVACVDVVEFTNQEVKEKEGFLRTYDCCVTTFQLEKSFRRVRINFNSPKSAARARIE 65  
 QY 117 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGVKPISDATPV 176  
 DB 66 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGVKPISDATPV 125  
 QY 177 LNYDLLYAVAKLPGGKYLHAGTSTPSVHVHVCSDMEREDPKTSPKPKINQTRRPG 236  
 DB 126 LNYDLLYAVAKLPGGKYLHAGTSTPSVHVHVCSDMEREDPKTSPKPKINQTRRPG 185  
 QY 237 LPP 239  
 DB 186 LPP 188

RESULT 8  
 ADE37341  
 ID ADE37341 standard; protein; 192 AA.  
 XX  
 AC ADE37341;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Down syndrome critical region 1-like 1 protein.  
 XX  
 KW Down syndrome critical region 1-like lalpa protein; nontropic;  
 KW neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;  
 KW human; Down syndrome critical region 1-like 1 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003186333-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 06-NOV-2002; 2002US-00290438.  
 XX  
 PR 11-JUL-2000; 2000US-00614474.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Loring JP, Tingley DW, Edwards CM, Streeter DG;  
 XX  
 DR WPI; 2003-811734/76.  
 XX  
 PT New purified Down syndrome critical region 1-like 1 protein, used for

PT diagnosing and treating Alzheimers disease, and for identifying and  
PT purifying antibodies that specific bind to the protein.  
XX  
PS Disclosure; SEQ ID NO 10; 39pp; English.  
XX  
XX This invention relates to a novel purified Down syndrome critical region  
CC 1-like 1 protein comprising a polypeptide having fully defined sequence  
CC of 255 amino acids, as given in the specification. Compounds which  
CC modulate the protein of the invention may have neurotropic or  
CC neuroprotective activity. The protein sequence of the invention and the  
CC cDNA sequence which encodes it may be useful for peptide therapy and gene  
CC therapy respectively. The invention may prove useful in development of  
CC therapeutics for the treatment of Alzheimer's disease. The present  
CC sequence is the amino acid sequence of the human Down syndrome critical  
CC region 1-like 1 protein which was used to demonstrate homology to the Down  
CC syndrome critical region 1-like 1alpha protein of the invention.  
XX  
SQ Sequence 192 AA;  
Query Match 65.4%; Score 848; DB 7; Length 192;  
Best Local Similarity 88.0%; Pred. No. 2.1e-81;  
Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;  
QY 57 NSLFCNVHQSVEEESKEFGLFRTYDECVTQLFKSFRVRINFNSHPKSAARARIE 116  
DB 6 STLVACVDVVEFTNQEVKEKGGFLRTYDDCVTFQLFKSFRVRINFNSHPKSAARARIE 65  
QY 117 LHETQFRGKKLPLYFAQVQTPETDGDGLHAPPQPAKQFLISPPSPSVGWKPISDATPV 176  
DB 66 LHETQFRGKKLPLYFAQVQTPETDGDGLHAPPQPAKQFLISPPSPSVGWKPIINDATPV 125  
QY 177 LNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTSPKPKINQTRRPG 236  
DB 126 LNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDIEBEDPKTSPKPKIIQTRRPG 185  
QY 237 LPP 239  
DB 186 LPP 188  
RESULT 9  
AAE18917  
ID AAE18917 standard; protein; 241 AA.  
XX  
AC AAE18917;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human MCIP associated protein #4.  
XX  
XX Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
KW heart failure; cardiomyopathy; heart disease; human.  
XX  
XX Homo sapiens.  
XX  
XX WO200204491-A2.  
XX  
XX 17-JAN-2002.  
XX  
XX 06-JUL-2001; 2001WO-US021662.  
XX  
XX 07-JUL-2000; 2000US-0216601P.  
XX  
XX 13-FEB-2001; 2001US-00782953.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA (WILL/) WILLIAMS S R.  
PA (ROTH/) ROTHERMEL B.  
XX  
XX Williams SR, Rothermel B;  
XX  
XX WPI; 2002-179698/23.  
DR N-PSDB; AAD30158.  
XX

PT Screening for modulators of muscle calcineurin interacting protein (MCIP)  
PT binding, expression or phosphorylation, useful for treating cardiac  
PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a  
test compound.  
XX  
XX Example 1; Page 168-169; 174pp; English.  
XX  
XX The invention relates to muscle calcineurin interacting proteins (MCIPs)  
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical  
CC complex with the catalytic subunit of calcineurin and increased levels of  
CC MCIPs correspond to a reduced ability of calcineurin to stimulate  
CC transcription of certain target genes. The invention also relates to  
CC methods for identifying modulators of MCIP binding, expression or  
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin  
CC may be used for treating cardiac hypertrophy and heart failure.  
CC Antibodies to MCIP can be used in characterising the MCIP content of  
CC healthy and diseased tissues and subsequently for determining the  
CC presence or absence of cardiomyopathy or as predictor of heart disease.  
CC The present sequence is human MCIP associated protein. Note: This  
CC sequence has been described as splice variant of MCIP1 initiated by exon  
CC 4 in the specification, however the sequence seems to be a MCIP  
CC associated protein  
XX  
SQ Sequence 241 AA;  
Query Match 54.7%; Score 708.5; DB 5; Length 241;  
Best Local Similarity 66.2%; Pred. No. 1.9e-66;  
Matches 141; Conservative 20; Mismatches 49; Indels 3; Gaps 2;  
QY 28 LCCIDRDWAVTQCF--EEAQAALTDGDLNLSLFCNVHQSVEEESKEKFEGLFRTY 85  
DB 16 LCSTDQEEEMIFGNEEDDLDEMDLSDLPSTLSLFCNVHQAFAVFEARQKGFALFTIY 75  
QY 86 DECVTQFLFKSFRVRINFNSHPKSAARARIELHETQFRGKKLPLYFAQVQTPETDGDGLH 145  
DB 76 DDQVTFQLFKSFRVRINFNSHPKSAARARIELHETDFTNGQKLPLYFAQVQMSGEVRDKSY 135  
QY 146 LAPPOPAKQFLISPPSPSVGWKPISDATPVNLVDLLYAVAKLGPGEKYLHAGTSTPS 205  
DB 136 LLPQPVRQFLISPPSPSVGWKQSEDAMPVINYDLLCAVSKLGPGEKYLHAGTSTPS 195  
QY 206 VVVHVCDSDMEREDPKTSPKPKINQTRRPGIP 238  
DB 196 VVVHVCESETEEBETK-NPKQIAQTRRPP 227  
RESULT 10  
ABO07173  
ID ABO07173 standard; protein; 241 AA.  
XX  
AC ABO07173;  
XX  
DT 13-AUG-2003 (first entry)  
XX  
XX Human p53 modifying protein, SEQ ID 133.  
XX  
XX Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;  
KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;  
KW lung cancer; ovarian cancer; angiogenesis; cell cycle;  
KW apoptotic disorder; cell proliferation disorder.  
XX  
XX Homo sapiens.  
XX  
XX WO200299122-A1.  
XX  
XX 12-DEC-2002.  
XX  
XX 03-JUN-2002; 2002WO-US017382.  
XX  
XX 05-JUN-2001; 2001US-0296076P.  
PR 10-OCT-2001; 2001US-0328605P.  
PR 15-FEB-2002; 2002US-0357253P.  
XX





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QY 55 LPNSLFACNVHQSVFEEESKEKFEGLFRITYDECVTFQLFKSPRRVRINFSPKSAAR 114
Db 64 LPSATTACHLDPRVFDVGLCKRAKESLFRITYDKDITFQYFKSPKRVIRINFSPFSAADAR 123
QY 115 IELHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQAKOFLISPPSSVGVKPI 174
Db 124 LQLHKEFLGKEMKLYFAQTLHGSS----HLAPPNPDQKFLISPPASPPVGWKQVEDAT 179
QY 175 PVLYNYDLLVAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PKPKIN 230
Db 180 PVLYNYDLLVAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PKPKIN 230
QY 231 QTRRPGLPP 239
Db 240 QTRRPVPT 248

RESULT 14
AAE18915
ID AAE18915 standard; protein; 197 AA.
XX AC AAE18915;
XX AC AAE18915;
DT 17-MAY-2002 (first entry)
DE Human MCIP associated protein #2.
XX XX
KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
KW heart failure; cardiomyopathy; heart disease; human.
XX OS Homo sapiens.
XX XX
PN WO200204491-A2.
XX PD 17-JAN-2002.
XX PF 06-JUL-2001; 2001WO-US021662.
XX PR 07-JUL-2000; 2000US-0216601P.
XX PR 13-FEB-2001; 2001US-00782953.
XX XX
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (WILL/) WILLIAMS S R.
PA (ROTH/) ROTHERMEL B.
XX PI Williams SR, Rothermel B;
XX WPI; 2002-179698/23.
XX DR N-PSDB; AAD30156.
XX XX
PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
PT binding, expression or phosphorylation, useful for treating cardiac
PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
PT test compound.
XX PS
XX Example 1; Page 161-162; 174pp; English.
XX XX
CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
CC complex with the catalytic subunit of calcineurin and increased levels of
CC MCIPs correspond to a reduced ability of calcineurin to stimulate
CC transcription of certain target genes. The invention also relates to
CC methods for identifying modulators of MCIP binding, expression or
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
CC may be used for treating cardiac hypertrophy and heart failure.
CC Antibodies to MCIP can be used in characterizing the MCIP content of
CC healthy and diseased tissues and subsequently for determining the
CC presence or absence of cardiomyopathy or as predictor of heart disease.
CC The present sequence is human MCIP associated protein. Note: This
CC sequence has been described as murine MCIP splice variant in the
CC specification, however the sequence seems to be a MCIP associated protein
XX SQ Sequence 197 AA;
```

```
Query Match 47.5%; Score 616; DB 5; Length 197;
Best Local Similarity 61.1%; Pred. No. 9.8e-57;
Matches 118; Conservative 28; Mismatches 39; Indels 8; Gaps 2;

QY 51 DFSDLNSLPACNVHQSVFEEESKEKFEGLFRITYDECVTFQLFKSPRRVRINFSPKSA 110
Db 5 DLQDLPSATTACHLDPRVFDVGLCKRAKESLFRITYDKDITFQYFKSPKRVIRINFSPFSA 64
QY 111 APARTLHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQAKOFLISPPSSVGVKPI 170
Db 65 ADARLQLHKEFLGKEMKLYFAQTLHGSS----HLAPPNPDQKFLISPPASPPVGWKQV 120
QY 171 SDATPVLYNYDLLVAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PK 226
Db 121 EDATPVLYNYDLLVAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PK 226
QY 227 PKINQTRRPGLPP 239
Db 181 PKIQTTRRPVPT 193

RESULT 15
AAE18914
ID AAE18914 standard; protein; 197 AA.
XX AC AAE18914;
XX AC AAE18914;
DT 17-MAY-2002 (first entry)
DE Human MCIP associated protein #1.
XX XX
KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
KW heart failure; cardiomyopathy; heart disease; human.
XX OS Homo sapiens.
XX XX
PN WO200204491-A2.
XX PD 17-JAN-2002.
XX PF 06-JUL-2001; 2001WO-US021662.
XX PR 07-JUL-2000; 2000US-0216601P.
XX PR 13-FEB-2001; 2001US-00782953.
XX XX
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (WILL/) WILLIAMS S R.
PA (ROTH/) ROTHERMEL B.
XX PI Williams SR, Rothermel B;
XX WPI; 2002-179698/23.
XX DR N-PSDB; AAD30155.
XX XX
PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
PT binding, expression or phosphorylation, useful for treating cardiac
PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
PT test compound.
XX PS
XX Example 1; Page 157-158; 174pp; English.
XX XX
CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
CC complex with the catalytic subunit of calcineurin and increased levels of
CC MCIPs correspond to a reduced ability of calcineurin to stimulate
CC transcription of certain target genes. The invention also relates to
CC methods for identifying modulators of MCIP binding, expression or
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
CC may be used for treating cardiac hypertrophy and heart failure.
CC Antibodies to MCIP can be used in characterising the MCIP content of
CC healthy and diseased tissues and subsequently for determining the
CC presence or absence of cardiomyopathy or as predictor of heart disease.
CC The present sequence is human MCIP associated protein. Note: This
CC sequence has been described as murine MCIP splice variant in the
CC specification, however the sequence seems to be a MCIP associated protein
XX SQ Sequence 197 AA;
```

CC The present sequence is human MCIP associated protein. Note: This  
CC sequence has been described as murine splice variant in the  
CC specification, however the sequence seems to be a MCIP associated protein  
XX  
SQ Sequence 197 AA;

Query Match 47.5%; Score 616; DB 5; Length 197;  
Best Local Similarity 62.8%; Pred. No. 9.8e-57;  
Matches 117; Conservative 27; Mismatches 35; Indels 8; Gaps 2;  
QY 57 NSLFCNVHQSVFEEESKEKEFGLRPTDYDECVTOLFYSFRVRINFSHPKSAARARIE 116  
Db 11 SLLIACVANSDFSESETRAKFESLRTYDKDITFQYFKSFKVRINFSNPFSAADARLQ 70  
QY 117 LHETQPRGKLLPLYFAQVQTPETDGDKLHLAPPQPAKQFLISPPSPSYGWKPISDATPV 176  
Db 71 LHKTEFLGKMKLYFAQTLHIGSS----HLAPPNDKQLISPPASPPYGVWKQVEDATPV 126  
QY 177 LNYDLIYAVAKLGPGKYLHAGTESTPSVVVHVCDSDMEREEDPKTS-----PKPKINOT 232  
Db 127 INYDLLYAIISKLGPGKYLHAAATDTPSVVVHVCSDOKEKEEEMERMRRPKKIQT 186  
QY 233 RRPGLPP 239  
Db 187 RREYTP 193

Search completed: November 16, 2005, 16:47:32  
Job time : 126.95 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:55 ; Search time 33 Seconds  
(without alignments)  
547.426 Million cell updates/sec

Title: US-09-575-580B-5  
Perfect score: 1296  
Sequence: 1 EFVDPRVRRLGQASIP.....TSPKINQTRRGLPPFGH 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
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5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1129	87.1	255	4	US-09-614-474-2 Sequence 2, Appli
2	861	66.4	206	4	US-09-949-016-11450 Sequence 11450, A
3	848	65.4	192	4	US-09-614-474-10 Sequence 10, Appl
4	848	65.4	192	4	US-09-949-016-6659 Sequence 6659, Ap
5	708.5	54.7	241	4	US-09-614-474-11 Sequence 11, Appl
6	708.5	54.7	248	4	US-09-949-016-7081 Sequence 7081, Ap
7	575	44.4	171	4	US-09-949-016-6493 Sequence 6493, Ap
8	575	44.4	173	4	US-09-949-016-11053 Sequence 11053, A
9	565	43.6	171	2	US-08-665-040-2 Sequence 2, Appli
10	405.5	31.3	289	4	US-09-270-767-44503 Sequence 44503, A
11	312	24.1	111	4	US-09-513-999C-5849 Sequence 5849, Ap
12	106.5	8.2	285	4	US-09-248-796A-19049 Sequence 19049, A
13	106.5	8.2	767	4	US-09-248-796A-15612 Sequence 15612, A
14	94	7.3	655	3	US-09-347-833-4 Sequence 4, Appli
15	89	6.9	905	2	US-08-574-959A-9 Sequence 9, Appli
16	89	6.9	905	3	US-09-357-014-9 Sequence 9, Appli
17	89	6.9	1135	2	US-08-574-959A-7 Sequence 7, Appli
18	89	6.9	1135	3	US-09-357-014-7 Sequence 7, Appli
19	88.5	6.8	782	4	US-09-252-991A-30464 Sequence 30464, A
20	88.5	6.8	4019	4	US-09-854-133-425 Sequence 425, App
21	85	6.6	454	3	US-08-348-518C-4 Sequence 4, Appli
22	85	6.6	454	3	US-08-476-509B-4 Sequence 4, Appli
23	84.5	6.5	1106	1	US-08-180-195-2 Sequence 2, Appli
24	84.5	6.5	1106	1	US-08-188-317-2 Sequence 2, Appli
25	84.5	6.5	1106	1	US-08-477-329-2 Sequence 2, Appli
26	84.5	6.5	1106	2	US-08-475-458-2 Sequence 2, Appli
27	84.5	6.5	1106	2	US-08-460-510-2 Sequence 2, Appli

28	84.5	6.5	1106	2	US-08-460-490-2	Sequence 2, Appli
29	84.5	6.5	1106	3	US-08-980-400-2	Sequence 2, Appli
30	84.5	6.5	1106	3	US-08-462-728-4	Sequence 2, Appli
31	84.5	6.5	1106	3	US-09-583-459A-2	Sequence 2, Appli
32	84.5	6.5	1106	3	US-09-583-210-2	Sequence 2, Appli
33	84.5	6.5	1106	3	US-09-583-449A-2	Sequence 2, Appli
34	84.5	6.5	1106	3	US-09-435-059-2	Sequence 2, Appli
35	84.5	6.5	1106	3	US-08-461-917-4	Sequence 4, Appli
36	84.5	6.5	1106	4	US-08-464-436-4	Sequence 4, Appli
37	84.5	6.5	1106	4	US-08-464-436-4	Sequence 4, Appli
38	84.5	6.5	1106	4	US-09-866-510-16	Sequence 16, Appl
39	84.5	6.5	1106	4	US-09-866-510-18	Sequence 18, Appl
40	84.5	6.5	1106	4	US-09-866-510-20	Sequence 20, Appl
41	84.5	6.5	1106	4	US-09-866-510-22	Sequence 22, Appl
42	84.5	6.5	1106	5	PCT-US92-00730-2	Sequence 2, Appli
43	84.5	6.5	1106	5	PCT-US92-00862-2	Sequence 2, Appli
44	84	6.5	428	3	US-09-347-833-6	Sequence 6, Appli
45	83	6.4	566	1	US-08-810-116-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-614-474-2  
; Sequence 2, Application US/09614474  
; Patent No. 6524819  
; GENERAL INFORMATION:  
; APPLICANT: Loring, Jeanne F.  
; APPLICANT: Tingley, Debra W.  
; APPLICANT: Edwards, Carla M.  
; APPLICANT: Streeter, David G.  
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION. 1-LIKE PROTEINS  
; FILE REFERENCE: PC-0013 US  
; CURRENT APPLICATION NUMBER: US/09/614,474  
; CURRENT FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6524819 247500.5  
; NAME/KEY: unsure  
; LOCATION: 11  
; OTHER INFORMATION: unknown or other  
US-09-614-474-2

Query Match	87.1%	Score 1129;	DB 4;	Length 255;
Best Local Similarity	92.5%	Pred. No. 1.5e-121;		
Matches	209;	Conservative	9;	Mismatches 8;
				Indels 0;
				Gaps 0;
QY	14	GQASIPEDGGLPFLCCIDRDMAVTCFAEEAFQALTFSDLSLFCNVHQSVEEEE	73	
Db	26	GQGHVPEDGGLPFLCCIDRDMAVTCFAEEAFQALTFSDLSLFCNVHQSVEEEE	85	
QY	74	SKEKFGRLRTYDECVTTFQLFKSFRRVRINFSPKSAARARIELHETQFRGKGLPLYFAQ	133	
Db	86	SKEKFGRLRTYDDCVTFQLFKSFRRVRINFSPKSAARARIELHETQFRGKGLPLYFAQ	145	
QY	134	VQPTETDGLKHLAPPQAPKQFLISPPSSPVGMKPSDATPVNLYLLVAVAKLGPGEK	193	
Db	146	VQPTETDGLKHLAPPQAPKQFLISPPSSPVGMKPSDATPVNLYLLVAVAKLGPGEK	205	
QY	194	YELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINQTRRGLPP	239	
Db	206	YELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINQTRRGLPP	251	

RESULT 2  
US-09-949-016-11450

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; Sequence 11450, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11450
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11450

Query Match 66.4%; Score 861; DB 4; Length 206;
Best Local Similarity 89.1%; Pred. No. 8.3e-91; Indels 0; Gaps 0;
Matches 163; Conservative 8; Mismatches 12;

QY 57 NSLFACNVHQSVFEEESKEFGLFRTYDECVTQFLFKSFRRVRINFSPKSAARARIE 116
Db 20 STLAVCVVDVEFTNQEVKEFGLFRTYDCVTQFLFKSFRRVRINFSPKSAARARIE 79
QY 117 LHETQFRGKKLPLYPFAQVQTPETDGDKLHLAPPQPAKQFLISPPSSPSVGWKPISDATPV 176
Db 80 LHETQFRGKKLPLYPFAQVQTPETDGDKLHLAPPQPAKQFLISPPSSPSVGWKPISDATPV 139
QY 177 LNYDLLYAVAKLGPGEKVELHAGTSTPSVVVHVCDSDMEREDPKTSFKPKINOTRRPG 236
Db 140 LNYDLLYAVAKLGPGEKVELHAGTSTPSVVVHVCDSDMEREDPKTSFKPKINOTRRPG 199
QY 237 LPP 239
Db 200 LPP 202

RESULT 3
US-09-614-474-10
; Sequence 10, Application US/09614474
; Patent No. 6524819
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6524819 gl435040
; US-09-614-474-10

Query Match 65.4%; Score 848; DB 4; Length 192;
Best Local Similarity 88.0%; Pred. No. 2.3e-89;
Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 57 NSLFACNVHQSVFEEESKEFGLFRTYDECVTQFLFKSFRRVRINFSPKSAARARIE 116
Db 20 STLAVCVVDVEFTNQEVKEFGLFRTYDCVTQFLFKSFRRVRINFSPKSAARARIE 65
QY 117 LHETQFRGKKLPLYPFAQVQTPETDGDKLHLAPPQPAKQFLISPPSSPSVGWKPISDATPV 176
Db 66 LHETQFRGKKLPLYPFAQVQTPETDGDKLHLAPPQPAKQFLISPPSSPSVGWKPISDATPV 125
QY 177 LNYDLLYAVAKLGPGEKVELHAGTSTPSVVVHVCDSDMEREDPKTSFKPKINOTRRPG 236
Db 126 LNYDLLYAVAKLGPGEKVELHAGTSTPSVVVHVCDSDMEREDPKTSFKPKINOTRRPG 185
QY 237 LPP 239
Db 186 LPP 188

RESULT 4
US-09-949-016-6659
; Sequence 6659, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6659
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6659

Query Match 65.4%; Score 848; DB 4; Length 192;
Best Local Similarity 88.0%; Pred. No. 2.3e-89;
Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 57 NSLFACNVHQSVFEEESKEFGLFRTYDECVTQFLFKSFRRVRINFSPKSAARARIE 116
Db 6 STLAVCVVDVEFTNQEVKEFGLFRTYDCVTQFLFKSFRRVRINFSPKSAARARIE 65
QY 117 LHETQFRGKKLPLYPFAQVQTPETDGDKLHLAPPQPAKQFLISPPSSPSVGWKPISDATPV 176
Db 66 LHETQFRGKKLPLYPFAQVQTPETDGDKLHLAPPQPAKQFLISPPSSPSVGWKPISDATPV 125
QY 177 LNYDLLYAVAKLGPGEKVELHAGTSTPSVVVHVCDSDMEREDPKTSFKPKINOTRRPG 236
Db 126 LNYDLLYAVAKLGPGEKVELHAGTSTPSVVVHVCDSDMEREDPKTSFKPKINOTRRPG 185
QY 237 LPP 239
Db 186 LPP 188

RESULT 5
US-09-614-474-11
; Sequence 11, Application US/09614474
; Patent No. 6524819
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
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; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6524819
US-09-614-474-11

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RESULT 6
US-09-949-016-7081
; Sequence 7081, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7081
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7081

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Qy      206  VVHVCDMEREEDPKTSPKPKINQTRRGLP 238
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Db      203  VVHVCESTEEEEK-NPKQKAQTRRPPPP 234

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RESULT 7  
US-09-949-016-6493  
; Sequence 6493, Application US/09949016  
; Patent NO. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6493  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6493

RESULT 8  
US-09-949-016-11053  
; Sequence 11053, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11053  
; LENGTH: 173  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11053





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QY 239 -----PFCH 242
Db 488 GRRAGTGGIQQPMPMCH 504

RESULT 15
US-08-574-959A-9
; Sequence 9, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 905 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-959A-9

Query Match 6.9%; Score 89; DB 2; Length 905;
Best Local Similarity 24.0%; Pred. No. 0.66;
Matches 41; Conservative 16; Mismatches 82; Indels 32; Gaps 5;

QY 70 EEESKEKPEGLFRTYDECVTQLFKSPRRVRINFSPKSAARARIELHETQFRGKLP 129
Db 698 EEEEEERFEFEFEEG-----ELEEEEEDEEEEEELEVE----- 736
QY 130 YFAQVQTPTDGDKHLHAPPQAKFLISPPSSPSVGWKPISDATPVLNLDLYAVAKLG 189
Db 737 ---DLEFGTAGGEVEGAPPTLPALPPESP-----PKVQPEPEPEPGILLVEE-- 786
QY 190 PGKEYELHAGTSTPSVVHVHCDSDMERE-EDPKTSPKPKINQTRRRPGLPP 239
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Job time : 34 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:57 ; Search time 123.2 Seconds  
(without alignments)  
821.876 Million cell updates/sec

Title: US-09-575-580B-5

Perfect score: 1296

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Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/FCRUS\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1129	87.1	243	US-10-104-047-2216
2	1129	87.1	255	US-10-290-438-2
3	882	68.1	197	US-09-782-953-9
4	882	68.1	197	US-09-782-953-10
5	848	65.4	192	US-09-782-953-18
6	848	65.4	192	US-09-782-953-19
7	848	65.4	192	US-10-290-438-10
8	848	65.4	197	US-10-764-425-126
9	708.5	54.7	241	US-09-782-953-21
10	708.5	54.7	241	US-09-782-953-22
11	708.5	54.7	241	US-10-290-438-11

12	676.5	52.2	212	9	US-09-782-953-24	Sequence 24, Appl
13	676.5	52.2	212	9	US-09-782-953-25	Sequence 25, Appl
14	648	50.0	252	15	US-10-104-047-2892	Sequence 2892, Ap
15	616	47.5	197	9	US-09-782-953-12	Sequence 12, Appl
16	616	47.5	197	9	US-09-782-953-13	Sequence 13, Appl
17	616	47.5	197	9	US-09-782-953-15	Sequence 15, Appl
18	616	47.5	197	9	US-09-782-953-16	Sequence 16, Appl
19	616	47.5	197	14	US-10-247-671-174	Sequence 174, Appl
20	616	47.5	197	16	US-10-755-889-120	Sequence 120, Appl
21	613.5	47.3	198	9	US-09-782-953-6	Sequence 6, Appl
22	613.5	47.3	198	9	US-09-782-953-7	Sequence 7, Appl
23	606.5	46.8	198	9	US-09-782-953-3	Sequence 3, Appl
24	606.5	46.8	198	9	US-09-782-953-4	Sequence 4, Appl
25	575	44.4	171	15	US-10-428-487-24	Sequence 24, Appl
26	418.5	32.3	292	20	US-11-097-143-41193	Sequence 41193, A
27	289	22.3	142	9	US-09-925-302-790	Sequence 790, App
28	289	22.3	142	10	US-09-925-302-790	Sequence 790, App
29	213	16.4	58	9	US-09-864-761-35379	Sequence 35379, A
30	213	16.4	58	9	US-09-864-761-43076	Sequence 43076, A
31	168	13.0	56	9	US-09-864-761-34111	Sequence 34111, A
32	101	7.8	32	14	US-10-194-155-8	Sequence 8, Appli
33	98.5	7.6	608	17	US-10-732-923-13425	Sequence 13425, A
34	98.5	7.6	922	15	US-10-042-865-96	Sequence 96, Appl
35	98.5	7.6	922	15	US-10-263-929-190	Sequence 190, App
36	98.5	7.6	948	13	US-10-087-192-1869	Sequence 1869, Ap
37	98.5	7.6	1066	15	US-10-042-865-95	Sequence 95, Appl
38	98.5	7.6	1066	17	US-10-732-923-13684	Sequence 13684, A
39	98.5	7.6	1077	17	US-10-732-923-13426	Sequence 13426, A
40	98.5	7.6	1096	15	US-10-210-130-130	Sequence 130, App
41	98.5	7.6	1097	15	US-10-288-798-12	Sequence 12, Appl
42	98.5	7.6	1097	15	US-10-362-892-12	Sequence 12, Appl
43	98.5	7.6	1118	15	US-10-112-944-259	Sequence 259, Appl
44	97.5	7.5	1024	15	US-10-042-865-16	Sequence 16, Appl
45	96.5	7.4	248	15	US-10-425-114-48915	Sequence 48915, A

#### ALIGNMENTS

RESULT 1  
US-10-104-047-2216  
; Sequence 2216, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2216  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2216

Query Match	87.1%	Score 1129;	DB 15;	Length 243;
Best Local Similarity	92.5%	Pred. No. 2.2e-105;		
Matches 209;	Conservative	9;	Mismatches 8;	Indels 0; Gaps 0;
QY	14	QQQASIPEDGGGLFFCCIDRDWAVTQCFAEAFQALTDPSDLPSLFCACNVHQSVEEBE	73	
Db	14	QQQGHVPEDGGGLFFCCIDRDWAVTQCFAEAFQALTDPSDLPSLFCACNVHQSVEEBE	73	
QY	74	SKEPEGLFRYDECVTFOLKFSRRVRINFSHPKSAARARIELHETQFRGKKLPLYFAQ	133	
Db	74	SKEPEGLFRYDDCVTFOLKFSRRVRINFSHPKSAARARIELHETQFRGKKLPLYFAQ	133	
QY	134	VQTPETDGDGLHAPPQPAKQFLISPPSSPSVGMKPISDATPVNLNLDLYAVAKLPGGEK	193	

Db 134 VOTPETDGDKLHAPPQAKQFLISPPSPVGVQWQPIN DATPVLNVDLLYAVAKLGPGEK 193  
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINQTRRGLPP 239  
Db 194 YELHAGTESTPSVVHVCDSDIEEREDPKTSPKPKIQTTRRGLPP 239

## RESULT 2

US-10-290-438-2  
; Sequence 2, Application US/10290438  
; Publication No. US20030186333A1  
; GENERAL INFORMATION:  
; APPLICANT: Loring, Jeanne P.  
; APPLICANT: Tingley, Debora W.  
; APPLICANT: Edwards, Carla M.  
; APPLICANT: Streeter, David G.  
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEIN  
; FILE REFERENCE: PC-0013-1CIP  
; CURRENT APPLICATION NUMBER: US/10/290,438  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 09/614,474  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030186333A1 247500.5  
; FEATURE:  
; LOCATION: 11  
; OTHER INFORMATION: unknown or other  
US-10-290-438-2

Query Match 87.1%; Score 1129; DB 14; Length 255;  
Best Local Similarity 92.5%; Pred. No. 2.3e-105;  
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
QY 14 GQAQSIPEGGFLFCLCCIDRDWAVTQCAEAEAFQALTFPSDLNLSFACNVHQSVFEE 73  
Db 26 GQQGHVPEDGGFLFCLCCIDRDWAVTQCAEAEAFQAITFDNLPSLFAACNVHQSVFEE 85  
QY 74 SKEFEGFLRTYDECVTQFLFKSPRRVRINFSPKSAARARIELHETQFRGKKLPLFYAQ 133  
Db 86 SKEFEGFLRTYDCCVTQFLFKSPRRVRINFSPKSAARARIELHETQFRGKKLPLFYAQ 145  
QY 134 VOTPETDGDKLHAPPQAKQFLISPPSPVGVQWQPIN DATPVLNVDLLYAVAKLGPGEK 193  
Db 146 VOTPETDGDKLHAPPQAKQFLISPPSPVGVQWQPIN DATPVLNVDLLYAVAKLGPGEK 205  
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINQTRRGLPP 239  
Db 206 YELHAGTESTPSVVHVCDSDIEEREDPKTSPKPKIQTTRRGLPP 251

## RESULT 3

US-09-782-953-9  
; Sequence 9, Application US/09782953  
; Patent No. US20020150953A1  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, R. SANDERS  
; APPLICANT: ROTHERMEL, BEVERLY  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
; FILE REFERENCE: UTSD:674P21  
; CURRENT APPLICATION NUMBER: US/09/782,953  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/216,601  
; PRIOR FILING DATE: 2000-07-07  
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 197  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-782-953-9

Query Match 68.1%; Score 882; DB 9; Length 197;  
Best Local Similarity 91.8%; Pred. No. 1.5e-80;  
Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;  
QY 57 NSLFACNVHQSVFEEESKEFEGFLRTYDECVTQFLFKSPRRVRINFSPKSAARARIE 116  
Db 11 STLAVACVVDVEFTNQEVKKEFEGFLRTYDECVTQFLFKSPRRVRINFSPKSAARARIE 70  
QY 117 LHETQFRGKKLPLFYAQVQTPTDGDKLHAPPQAKQFLISPPSPVGVQWQPIN DATPV 176  
Db 71 LHETQFRGKKLPLFYAQVQTPTDGDKLHAPPQAKQFLISPPSPVGVQWQPIN DATPV 130  
QY 177 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINQTRRPG 236  
Db 131 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSPKPKIQTTRRPG 190  
QY 237 LPP 239  
Db 191 LPP 193

## RESULT 4

US-09-782-953-10  
; Sequence 10, Application US/09782953  
; Patent No. US20020150953A1  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, R. SANDERS  
; APPLICANT: ROTHERMEL, BEVERLY  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
; FILE REFERENCE: UTSD:674P21  
; CURRENT APPLICATION NUMBER: US/09/782,953  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR FILING DATE: 60/216,601  
; PRIOR APPLICATION NUMBER: 2000-07-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 197  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-782-953-10  
Query Match 68.1%; Score 882; DB 9; Length 197;  
Best Local Similarity 91.8%; Pred. No. 1.5e-80;  
Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;  
QY 57 NSLFACNVHQSVFEEESKEFEGFLRTYDECVTQFLFKSPRRVRINFSPKSAARARIE 116  
Db 11 STLAVACVVDVEFTNQEVKKEFEGFLRTYDECVTQFLFKSPRRVRINFSPKSAARARIE 70  
QY 117 LHETQFRGKKLPLFYAQVQTPTDGDKLHAPPQAKQFLISPPSPVGVQWQPIN DATPV 176  
Db 71 LHETQFRGKKLPLFYAQVQTPTDGDKLHAPPQAKQFLISPPSPVGVQWQPIN DATPV 130  
QY 177 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSPKPKINQTRRPG 236  
Db 131 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSPKPKIQTTRRPG 190  
QY 237 LPP 239  
Db 191 LPP 193  
RESULT 5  
US-09-782-953-18







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Db 16 LCSTQEEBEMIFGENEDDLDEMMDLSLPTSLFACSVHEAVFEAREQKERFEALFTY 75
Qy 86 DECVTFQLFKSFRVRINFSHPKSAARARIELHETQFRGKPLYPFAQVOTPETDGDKLH 145
Db 76 DQVTFQLFKSFRVRINFSKPEAAARARIELHETDFNGQKLYFAQVQMSGEVDRKSY 135
Qy 146 LAPPOPAKQFLISPPSPSGVWKPISDATPVNLNLYLLYAVAKLPGCEKYLHAGTSTPS 205
Db 136 LPPQPVKQFLISPPSPSGVWKQSDAMPVINYDLLCAVSKLPGCEKYLHAGTSTPS 195
Qy 206 VVVHVCSDMEREEDPKTSPPKPKINOTRRPGLP 238
Db 196 VVVHVCESETEEBETK-NPKQKIAQTRRPDP 227
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RESULT 12
US-09-782-953-24
; Sequence 24, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: CALCINEURIN INTERACTING PROTEIN (MCIP)
; CURRENT APPLICATION NUMBER: US/09/782,953
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-24
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Query Match 52.2%; Score 676.5; DB 9; Length 212;
Best Local Similarity 67.9%; Pred. No. 9.5e-60;
Matches 133; Conservative 18; Mismatches 34; Indels 11; Gaps 2;

Qy 43 BEAFQALTDPSLPSLACNVHQSVEFEESKEKEGFLFRTYDECVTFQLFKSFRVRV 102
Db 14 EDDLDEMMDLSLPTSLFACSVHEAVFEAREQKERFEALFTYDQVTFQLFKSFRVR 73
Qy 103 NFSHPKSAARARIELHETQFRGKPLYPFAQVOTPETDGDKLHAPPQPAKQFLISPPSS 162
Db 74 NFSKPEAAARARIELHETDFNGQKLYFAQ-----SYLLPPQPVKQFLISPPAS 123
Qy 163 PSVGWKPISDATPVNLNLYLLYAVAKLPGCEKYLHAGTSTPSVVHVCDSDMEREEDPK 222
Db 124 PPGWKQSDAMPVINYDLLCAVSKLPGCEKYLHAGTSTPSVVHVCESETEEBETK 183
Qy 223 TSPKPKINOTRRPGLP 238
Db 184 -NPKQKIAQTRRPDP 198
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RESULT 13
US-09-782-953-25
; Sequence 25, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: CALCINEURIN INTERACTING PROTEIN (MCIP)
; CURRENT APPLICATION NUMBER: US/09/782,953
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2000-07-07
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-25
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Query Match 52.2%; Score 676.5; DB 9; Length 212;
Best Local Similarity 67.9%; Pred. No. 9.5e-60;
Matches 133; Conservative 18; Mismatches 34; Indels 11; Gaps 2;

Qy 43 BEAFQALTDPSLPSLACNVHQSVEFEESKEKEGFLFRTYDECVTFQLFKSFRVRV 102
Db 14 EDDLDEMMDLSLPTSLFACSVHEAVFEAREQKERFEALFTYDQVTFQLFKSFRVR 73
Qy 103 NFSHPKSAARARIELHETQFRGKPLYPFAQVOTPETDGDKLHAPPQPAKQFLISPPSS 162
Db 74 NFSKPEAAARARIELHETDFNGQKLYFAQ-----SYLLPPQPVKQFLISPPAS 123
Qy 163 PSVGWKPISDATPVNLNLYLLYAVAKLPGCEKYLHAGTSTPSVVHVCDSDMEREEDPK 222
Db 124 PPGWKQSDAMPVINYDLLCAVSKLPGCEKYLHAGTSTPSVVHVCESETEEBETK 183
Qy 223 TSPKPKINOTRRPGLP 238
Db 184 -NPKQKIAQTRRPDP 198
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RESULT 14
US-10-104-047-2892
; Sequence 2892, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2892
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2892
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Query Match 50.0%; Score 648; DB 15; Length 252;
Best Local Similarity 53.4%; Pred. No. 9.2e-57;
Matches 133; Conservative 30; Mismatches 58; Indels 28; Gaps 5;

Qy 1 EFDVPRVRPRV-----LGOQASIPEDGGLFFLCICIDRDMAVTQCFABEAFQALTD 54
Db 18 EAAEARARPGVTLRPFAPLSGAADAEDEGG-----DWSFIDCEMEE-----V 63
Qy 55 LPSLACNVHQSVEFEESKEKEGFLFRTYDECVTFQLFKSFRVRINFSHPKSAARAR 114
Db 64 LPSATIACHLDPRVFDGLCRAKFESLFRTYDKDITFQYFKSFRVRINFSNPFSAADAR 123
Qy 115 TELHETQFRGKPLYPFAQVOTPETDGDKLHAPPQPAKQFLISPPSPSGVWKPISDAT 174
Db 124 LQLHKTFLGEMKLYFAQTLHIGSS-----HLAPNPKQFLISPPSPSGVWKQVEDAT 179
Qy 175 PVLNLYLLYAVAKLPGCEKYLHAGTSTPSVVHVCDSDMEREEDPKTS-----PKPKIN 230
Db 180 PVINYDLLYAIKSLGPGCEKYLHAGTSTPSVVHVCESETEEBETK-----PKPKII 239
Qy 231 QTRRPGLP 239
Db 240 QTRREYTP 248
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Search completed: November 16, 2005, 16:53:29  
Job time : 124.2 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	330.5	25.5	239	2	T34305	hypothetical prote
2	132	10.2	315	2	T49641	nebula related pro
3	99.5	7.7	163	2	S62444	conserved hypothet
4	93.5	7.2	813	2	A72203	cellobiose-phospho
5	93	7.2	428	2	T32952	hypothetical prote
6	91.5	7.1	387	2	B84721	hypothetical prote
7	91	7.0	671	2	C96534	probable Poly-A Bi
8	90.5	7.0	1557	2	T13160	protein CNK - frui
9	90	6.9	277	2	T37629	hypothetical prote
10	88	6.8	160	2	C72706	hypothetical prote
11	87.5	6.8	563	2	I45611	hypothetical prote
12	87.5	6.8	736	2	JA0681	Mx protein - pig
13	86.5	6.7	1331	2	A48954	gephyrin - rat
14	86.5	6.7	3938	2	T42761	mannan endo-1,4-be
15	86.5	6.7	6831	2	A8852	Bassoon protein -
16	86.5	6.7	6839	2	S57242	protein unc-22 [im
17	86.5	6.7	7160	2	T27935	twitchin [similar
18	86	6.6	525	2	A99533	hypothetical prote
19	86	6.6	885	2	B70393	hypothetical prote
20	86	6.6	2526	2	T20531	hypothetical prote
21	85	6.6	454	2	A56954	yes-associated pro
22	85	6.6	698	2	JH0163	No-on-transient A
23	85	6.6	700	2	JH0162	No-on-transient A
24	84.5	6.5	457	2	S03961	Ig mu chain C regi
25	84.5	6.5	1106	1	PFHUGB	platelet-derived g
26	83.5	6.4	1444	2	B84809	hypothetical prote
27	83.5	6.4	3942	2	T42730	Bassoon protein -
28	83	6.4	1098	1	PFWSRB	platelet-derived g
29	82.5	6.4	1044	2	HW1049	translation initia



[illegible]

```

N;Alternate names: ksr connector enhancer protein
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13160
R;Therrien, M.; Wong, A.M.; Rubin, G.M.
Cell 95, 343-353, 1998
A;Title: CNK, a RAF-binding multidomain protein required for RAS signaling.
A;Reference number: Z17616; MUID:99029842; PMID:9814705
A;Accession: T13160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1557 <THE>
A;Cross-references: UNIPROT:O96652; EMBL:AF100152; NID:G3930778; PID:G3930779; PIDN:AAC
C;Genetics:
A;Cross-references: FlyBase:FBgn0021818
C;Function:
A;Description: regulates RAF function and/or targets RAF to a specific subcellular comp

Query Match 7.0%; Score 90.5; DB 2; Length 1557;
Best Local Similarity 24.2%; Pred.No.15;
Matches 47; Conservative 22; Mismatches 76; Indels 49; Gaps 8;

Qy 46 FQALTFPSDLPLNSLPACNVHQSVFEE-----SKEKEGLRTVD 86
Db 511 FDAKEDYV-MKNKFKFNVNTILETFPIPFADGEDDALETLRNCKTENABELLEAN 569

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Db 313 -----GQWKYNAIGTSSTPT-----STVTPTPTPTPTPTVATPTPTPT 357

RESULT 14

T42761

Basoon protein - rat

N:Alternate names: brain-specific synapse-associated protein

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T42761

R:Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex J. Cell Biol. 142, 499-509, 1998

A:Title: Basoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localizes to dendritic spines

A:Reference number: 222249; MUID:98345363; PMID:9679147

A:Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-3938 <DIE>

A:Cross-references: UNIPROT:O88778; EMBL:Y16563; MID:g3413503; PIDN:CAA76287.1; PID:g3413503

A:Experimental source: strain Sprague Dawley; brain

C:Function:

A:Description: may be involved in cytomatrix organization at the site of neurotransmission

A:Note: component of the presynaptic cytoskeleton

C:Keywords: coiled coil; zinc finger

Query Match 6.7%; Score 86.5; DB 2; Length 3938;

Best Local Similarity 30.4%; Pred. No. 1.1e+02;

Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7;

QY 132 AQQTPTETDGLHLAPPQAKOFLISPPSSPSGVKWKPISDATPVLNYDLLYAVAKLGP 191

DB 1441 ASREKPLUSGGDG-EVGPPQPSRGYSYFTGSP-----PLSPSTP--SESPTFSKLGP 1492

QY 192 ERYELHAGTES-TFSVVVHVCDMSEREEDPKTSPKPKINQ-----TRRPLP 238

DB 1493 ATAESTTQTPSLTPS-----SDIPRSVG---TPSPMVAQGQTTPHRPSTP 1534

RESULT 15

A88852

protein unc-22 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C:Accession: A88852

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects/C\_elegans/

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999

A:Accession: A88852

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6831 <STO>

A:Cross-references: UNIPROT:Q23550; GB:chr\_IV; PIDN:CAA98081.1; PID:g33881830; GSPDB:GNO

C:Genetics:

A:Gene: unc-22

A:Map position: 4

C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;

Query Match 6.7%; Score 86.5; DB 2; Length 6831;

Best Local Similarity 20.3%; Pred. No. 2.2e+02;

Matches 65; Conservative 28; Mismatches 102; Indels 125; Gaps 13;

QY 35 WAYTQCFAAEAFQALTFDSLPLNSLF-----ACNVHQSVEEESKEKF---- 78

DB 3856 WTVGDSGAALPELLVDAKSSTTSIFPSAKRADSGNYKLVKVKELGDEAIFEVIVQDR 3915

QY 79 -----EGLFR-----TYDECTVFLFKSRRVRINFSHPKSAARAIELHETQFGKK----- 126

DB 3916 PSAPGPLEVSDVTKDSCV-----LNWPKPKDGGGAEISNYVVEKRDTKNTW 3963



GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 16, 2005, 16:32:05 ; Search time 60.5 Seconds  
(without alignments)  
2048.317 Million cell updates/sec  
Title: US-09-575-580B-5  
Perfect score: 1296  
Sequence: 1 BFVDRVRPRVRLGQASIP.....TSPKPKINQTRRPGLPFGH 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1186	91.5	243	2	Q8VIP4 mus musculus
2	1176	90.7	243	2	Q8CH26 rattus norv
3	1116	86.1	243	2	Q8N116 homo sapien
4	882	68.1	197	1	CCP2_MOUSE
5	876	67.6	197	2	Q8CH27
6	868	67.0	192	2	Q8VIP5 mus musculus
7	861	66.4	225	2	Q86YJ0 homo sapien
8	848	65.4	197	1	CCP2_HUMAN
9	725	55.9	195	2	Q6NSN4 brachydanio
10	720.5	55.6	239	1	CCP3_MOUSE
11	708.5	54.7	241	1	CCP3_HUMAN
12	702	54.2	230	2	Q6DG39
13	648	50.0	252	2	Q72555
14	632	48.8	251	2	Q7TNY3
15	617	47.6	197	1	CCP1_CRIGR
16	616	47.5	197	1	CCP1_HUMAN
17	616	47.5	199	2	Q6IN33
18	615	47.5	197	2	Q6XXM7
19	614	47.4	199	2	Q8K4S2
20	608.5	47.0	198	1	CCP1_MOUSE
21	589	45.4	199	2	Q7T0U1
22	588	45.4	199	2	Q6DK90
23	582	44.9	242	2	Q6ZMM3
24	579	44.7	231	2	Q7ZXP4
25	540	41.7	196	2	Q6DGB1
26	522.5	40.3	210	2	Q6DC33
27	418.5	32.3	292	1	SRA_DROME
28	330.5	25.5	207	1	CCPL_CABEL
29	132	10.2	315	2	Q9P5S9
30	121.5	9.4	249	2	Q66PG0
31	116.5	9.0	249	2	Q9P4A1

32	115.5	8.9	264	2	Q6C6F1	Q6C6F1 yarrowia li
33	99.5	7.7	163	1	YASP_SCHPO	Q09791 schizosacch
34	98.5	7.6	608	2	Q8BI68	Q8BI68 mus musculus
35	98.5	7.6	732	2	Q8K2L2	Q8K2L2 mus musculus
36	98.5	7.6	1066	2	Q9H2N5	Q9H2N5 homo sapien
37	97.5	7.5	1104	2	Q6EH31	Q6EH31 homo sapien
38	97	7.5	282	2	Q6BT12	Q6BT12 debaryomyce
39	96.5	7.4	585	2	Q74ZS6	Q74ZS6 ashbya gosa
40	96.5	7.4	1097	1	PGDR_RAT	Q05030 rattus norv
41	95	7.3	479	2	Q9M6E4	Q9M6E4 nicotiana c
42	94	7.3	220	2	Q9FGA3	Q9FGA3 arabidopsis
43	94	7.3	660	2	Q6Z050	Q6Z050 oryza sativ
44	93.5	7.2	409	2	Q6CMZ1	Q6CMZ1 kluyveromyc
45	93.5	7.2	567	2	Q8G7Y8	Q8G7Y8 bifidobacte

ALIGNMENTS

RESULT 1

Q8VIP4	PRELIMINARY;	PRT;	243 AA.
AC	Q8VIP4;		
DT	01-MAR-2002 (Tremblrel. 20, Created)		
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)		
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)		
DE	Calcineurin inhibitory protein ZAKI-4 beta.		
GN	Name=Dscr111; Synonyms=ZAKI-4 beta;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kanou Y., Miyazaki T., Seo H., Murata Y.;		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB061525; BAB71956.1; -		
DR	MGD; MGI:1858219; Dscr111.		
DR	GO; GO:0019722; P;calcium-mediated signaling; IEA.		
DR	Pfam; PF04847; Calcipressin; 1.		
SQ	SEQUENCE 243 AA; 27332 MW; 2CD8C1A810291851 CRC64;		

Query Match	91.5%;	Score 1186;	DB 2;	Length 243;
Best Local Similarity	98.2%;	Pred. No. 8.8e-93;		
Matches	223;	Conservative	0;	Mismatches 4;
Indels	0;	Gaps	0;	
Qy	13	LQQAASIPEDGGLFLCCIDRDWAVTQCFABEAFQALTDPSDLNLSLFCACNVHQSVEEE	72	
Db	13	LQQAASIPEDGGLFLCCIDRDWAVTQCFABEAFQALTDPSDLNLSLFCACNVHQSVEEE	72	
Qy	73	ESKEKEGLFRYDSCVTFOLEKSFRRVRINFSHPKSAARARIELHETQFRGKKLPLYP	132	
Db	73	ESKEKEGLFRYDSCVTFOLEKSFRRVRINFSHPKSAARARIELHETQFRGKKLPLYP	132	
Qy	133	QVQTETDGDGLHAPPAPAKOFLISPPSSPVGVKPKISDAPVNLNLLYAVAKLGPGE	192	
Db	133	QVQTETDGDGLHAPPAPAKOFLISPPSSPVGVKPKISDAPVNLNLLYAVAKLGPGE	192	
Qy	193	KYELHAGTESTPSVVHVHVCDSMEEREEDPKTSPKPKINQTRRPGLP	239	
Db	193	KYELHAGTESTPSVVHVHVCDSMEEREEDPKTSPKPKINQTRRPGLP	239	

RESULT 2

Q8CH26	PRELIMINARY;	PRT;	243 AA.
ID	Q8CH26;		
AC	Q8CH26;		
DT	01-MAR-2003 (Tremblrel. 23, Created)		
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)		
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)		
DE	ZAKI-4 beta.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RA Miyazaki T., Cao X., Kambe F., Ohmori S., Seo H.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF459023; AAO15541.1; -.
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calcipressin.
DR Pfam; PF04847; Calcipressin; 1.
SQ SEQUENCE 243 AA; 27311 MW; 00E05BD1DCD0492D CRC64;

Query Match 90.7%; Score 1176; DB 2; Length 243;
Best Local Similarity 96.5%; Pred. No. 6.2e-92;
Matches 219; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 13 LQQASIPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDPSLNSLFACNVHQSVFEE 72
Db 13 LQQASVPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDNLPLNSLFACNVHQSVFEE 72

QY 73 ESKEFEGFLRTYDECVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 132
Db 73 ESKEFEGFLRTYDECVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 132

QY 133 QVQTPETDGDKLHLAPPQAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGE 192
Db 133 QVQTPETDGDKLHLAPPQAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGE 192

QY 193 KYELHAGTESPVSVVHVCDSDMEREDPKTSPKPKINQTRRPLPP 239
Db 193 KYELHAGTESPVSVVHVCDSDLEBEDPKTSPKPKIIQTRRPLPP 239

RESULT 3
ID Q8N116 PRELIMINARY; PRT; 243 AA.
AC Q8N116;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcineurin inhibitor ZAKI-4 beta splice variant 1 (Calcineurin
DE inhibitor ZAKI-4 beta splice variant 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22250686; PubMed=12102656; DOI=10.1042/BJ20011797;
RA Cao X., Kambe F., Miyazaki T., Sarkar D., Ohmori S., Seo H.;
RT "Novel human ZAKI-4 isoforms: hormonal and tissue-specific regulation
RT and function as calcineurin inhibitors.";
RL Biochem. J. 357:459-466(2002).
DR EMBL; AY034085; AAK59805.1; -.
DR EMBL; AY034086; AAK59806.1; -.
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calcipressin.
DR Pfam; PF04847; Calcipressin; 1.
SQ SEQUENCE 243 AA; 27247 MW; 780073AE29A973E4 CRC64;

Query Match 86.1%; Score 1116; DB 2; Length 243;
Best Local Similarity 91.6%; Pred. No. 7.9e-87;
Matches 207; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 14 GQASIPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDPSLNSLFACNVHQSVFEE 73
Db 14 GQASVPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDNLPLNSLFACNVHQSVFEE 73

QY 74 SKEKFEGLRTYDECVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 133
Db 74 SKEKFEGLRTYDVCVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 133
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QY 134 VQTPETDGDKLHLAPPQAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGEK 193
Db 134 VQTPETDGDKLHLAPPQAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGEK 193

QY 194 YELHAGTESPVSVVHVCDSDMEREDPKTSPKPKINQTRRPLPP 239
Db 194 YELHAGTESPVSVVHVCDSDIEBEDPKTSPKPKIIQTRRPLPP 239

RESULT 4
CCP2_MOUSE
ID CCP2_MOUSE STANDARD; PRT; 197 AA.
AC Q9JHG2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 2 (Down syndrome candidate region 1-like protein 1)
DE (Myocyte-enriched calcineurin interacting protein 2) (MCIP2).
GN Name=Dscr1l1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20187590; PubMed=10722714; DOI=10.1074/jbc.275.12.8719;
RA Rothermel B., Vega R.B., Yang J., Wu H., Bassel-Duby R.,
RA Williams R.S.;
RT "A protein encoded within the Down syndrome critical region is
RT enriched in striated muscles and inhibits calcineurin signaling.";
RL J. Biol. Chem. 275:8719-8725(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=20534792; PubMed=11080588; DOI=10.1016/S0378-1119(00)00407-8;
RA Striappoli P., Petrini M., Lenzi L., Carinci P., Zannotti M.;
RT "The murine DSCR1-like (Down syndrome candidate region 1) gene family:
RT conserved synteny with the human orthologous genes.";
RL Gene 257:223-232(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
CC by binding to the catalytic domain of calcineurin A. Could play a
CC role during central nervous system development.
CC -!- TISSUE SPECIFICITY: Highest expression in heart, skeletal muscle
CC and brain. Lower expression in all other tissues.
CC -!- SIMILARITY: Belongs to the DSCR1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC -----
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalil U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070010; AAH70010.1; -.
DR ZFIN; ZDB-GENE-040516-17; ZGC:85746.
DR GO; GO:0013722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; CalciPressin.
DR Pfam; PF04847; CalciPressin; 1.
SQ SEQUENCE 195 AA; 21775 MW; F4F4CEC9B9B4F8AA CRC64;

Query Match 55.9%; Score 725; DB 2; Length 195;
Best Local Similarity 75.8%; Pred. No. 1.1e-53;
Matches 138; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 57 NSLFCNVHQSVFEEESKEPEGLFRTYDECVTFLPKSPRRVINFSPKSAARATIE 116
DB 11 STLIACADVVEFTSEVKEMFEALFLAYDEGVTFOQKSPRRVINFSPKSAARATIE 70

QY 117 LHETQFRGKGLPLYFAQVQTPETDGLKLHAPPQPAKQLISPPSPSYGKPKISDATPV 176
DB 71 LHETQFRGKGLPLYFAQVQNPVSEGDNLHAPPQSPKQLISPPSPSYGKPKIDEATPV 130

QY 177 LNYDLLYAVAKLPGKEKYLHAGTSTPSVVHVCDSDMEREDPKTSKPKINQTRRP 236
DB 131 INYDLLYAVAKLPGKEKFLHAGTSTPSVVHVCDSDTDEEKPKNPKKIQTRRPD 190

QY 237 LP 238
DB 191 LP 192

RESULT 10
CCP3 MOUSE STANDARD; PRT; 239 AA.
AC Q9JXK0; Q9CX87;
AT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 3 (Down syndrome candidate region 1-like protein 2)
DE (Myocyte-enriched calcineurin interacting protein 3) (MCP3).
GN Name=Dscr1l2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=20534792; PubMed=11080588; DOI=10.1016/S0378-1119(00)00407-8;
RA Strippoli P., Petrini M., Lenzi L., Carinci P., Zannotti M.;
RT "The murine DSCR1-like (Down syndrome candidate region 1) gene family:
RT conserved synteny with the human orthologous genes.";
RL Gene 257:223-232(2000).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richardson S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalil U.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3].
RP SEQUENCE OF 40-239 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kani A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
CC by binding to the catalytic domain of calcineurin A. Could play a
CC role during central nervous system development (By similarity).
CC -!- SIMILARITY: Belongs to the DSCR1 family.
CC
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CC
CC EMBL; AF237888; AAF62539.1; -.
CC EMBL; BC059001; AAB59001.1; -.
CC EMBL; AK019377; BAB31687.1; -.
CC MGD; MGI:1858220; Dscr1l2.
CC InterPro; IPR006931; CalciPressin.
CC Pfam; PF04847; CalciPressin; 1.
SQ SEQUENCE 239 AA; 27153 MW; 1B2687B47BB4D272 CRC64;

Query Match 55.6%; Score 720.5; DB 1; Length 239;
Best Local Similarity 66.2%; Pred. No. 3.4e-53;
Matches 141; Conservative 23; Mismatches 46; Indels 3; Gaps 2;

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Db 124 LHKTEFLGKEMKLYFAQTUHGSS-----HLAPNPDKQLISPPASPPVGMKQVEDATPV 179
QY 177 LNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVHVCDSMDEREEDPK-----TSPKPKINQ 231
Db 180 INYDLLYALSKLGPGEKYLHAGTSTPSVVHVHVCDSMDEREEDPK-----TSPKPKINQ 231
QY 232 TRRPGGLPP 239
Db 240 TRPEYTP 247
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RESULT 15

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CCPI_CRIGR
ID CCPI_CRIGR STANDARD; PRT; 197 AA.
AC O35847;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 1 (Down syndrome critical region protein 1 homolog)
DE (Oxidative-induced protein Adapt78).
GN Name=DSCR1; Synonyms=ADAPT78;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97329095; PubMed=9185608; DOI=10.1006/abbi.1997.0109;
RA Crawford D.R., Leahy K.P., Abramova N., Lan L., Wang Y., Davies K.J.;
RT "Hamster adapt78 mRNA is a Down syndrome critical region homologue
RL Arch. Biochem. Biophys. 342:6-12(1997).
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
CC by binding to the catalytic domain of calcineurin A. Could play a
CC role during central nervous system development (By similarity).
CC -!- INDUCTION: By oxidative stress.
CC -!- SIMILARITY: Belongs to the DSCR1 family.
CC -----
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CC -----
DR EMBL; U60263; AB368517.1; -
DR InterPro; IPR006931; Calcipressin.
DR Pfam; PF04847; Calcipressin; 1.
SQ SEQUENCE 197 AA; 22674 MW; 0EFC68F55826439 CRC64;
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Query Match 47.6%; Score 617; DB 1; Length 197;
Best Local Similarity 62.2%; Pred. No. 1.7e-44;
Matches 120; Conservative 26; Mismatches 39; Indels 8; Gaps 2;
QY 51 DFSDLPLNSLFACNVHQSVEEESKEFGLFRTYDECVTQFLFKSFRVRVINFSPKSA 110
Db 5 DFNYNFSSLIACVANGDVFESESETRAKFESLFRTYDKDITQYFKSKRVINFSPKSA 64
QY 111 ABARIELHETQPRGKLLPYFAQVOTPETDGDKLHAPPQAKQFLISPPSPSVGWKPI 170
Db 65 ADARLQLHKTEFLGKEMKLYFAQTUHGSS-----HLAPNPDKQLISPPASPPVGMKQV 120
QY 171 SDATPVLNVDLLYAVAKLGPGEKYLHAGTSTPSVVHVHVCDSMDEREEDPKTS----PK 226
Db 121 EDATPVINYDLLYALSKLGPGEKYLHAGTSTPSVVHVHVCDSMDEREEDPKTS----PK 226
QY 227 PKINQTRRPGGLPP 239
Db 181 PKIQTTRPEYTP 193
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Search completed: November 16, 2005, 17:12:35  
Job time : 61.5 secs